

WHAT IS CLAIMED IS:

1. An isolated polynucleotide of an *Alloiococcus otitidis* genomic sequence, wherein the polynucleotide comprises a nucleotide sequence having at least about 70% identity to a nucleotide sequence chosen from one of odd numbered sequences from SEQ ID NO: 1 to SEQ ID NO: 6649, a complement thereof, a degenerate variant thereof, and a fragment thereof.
2. The polynucleotide of claim 1, wherein the polynucleotide is a complement to a nucleotide sequence chosen from one of odd numbered sequences from SEQ ID NO: 1 to SEQ ID NO: 6649, a complement thereof, a degenerate variant thereof, and a fragment thereof.
3. The polynucleotide of claim 2, wherein the polynucleotide is selected from the group consisting of genomic DNA, cDNA and RNA.
4. The polynucleotide of claim 3, wherein the polynucleotide further comprises heterologous nucleotides.
5. An isolated polynucleotide which hybridizes to a nucleotide sequence chosen from one of the odd numbered sequences from SEQ ID NO: 1 to SEQ ID NO: 6649, a complement thereof, a degenerate variant thereof, or a fragment thereof, under high stringency hybridization conditions.
6. The polynucleotide of claim 5, wherein the polynucleotide hybridizes under intermediate stringency hybridization conditions.
7. An isolated polynucleotide of an *Alloiococcus otitidis* genomic sequence, wherein the polynucleotide comprises a nucleotide sequence chosen from one of odd numbered sequences from SEQ ID NO: 1 to SEQ ID NO: 6649, a complement thereof, a fragment thereof, or a degenerate variant thereof, and encodes a polypeptide, a biological equivalent thereof, or a fragment thereof, and is selected from the group consisting of:

- (a) an *Alloiococcus otitidis* polypeptide predicted by SignalP algorithm analysis as having met all four criteria set out in the SignalP algorithm for a polypeptide having a signal peptide and predicted by HMM SignalP algorithm analysis as having a signal peptide;
- 5 (b) an *Alloiococcus otitidis* polypeptide predicted by SignalP algorithm analysis as having met three of the four criteria set out in the SignalP algorithm for a polypeptide having a signal peptide and predicted by HMM SignalP algorithm analysis as having a signal peptide;
- 10 (c) an *Alloiococcus otitidis* polypeptide predicted by HMM Signal P algorithm analysis as having a signal peptide;
- (d) an *Alloiococcus otitidis* polypeptide predicted by HMM Signal P algorithm analysis as being a non-secretory protein and by PSORT program to be localized to the cytoplasmic membrane;
- (e) an *Alloiococcus otitidis* polypeptide identified by BlastP analysis;
- 15 (f) an *Alloiococcus otitidis* polypeptide identified by Pfam analysis;
- (g) an *Alloiococcus otitidis* polypeptide identified using proteomics methodology as sharing homology with surface exposed proteins of *Streptococcus pneumoniae*;
- (h) an *Alloiococcus otitidis* lipoprotein;
- 20 (i) an *Alloiococcus otitidis* polypeptide having a LPXTG motif, wherein the polypeptide is covalently attached to the peptidoglycan layer;
- (j) an *Alloiococcus otitidis* polypeptide, wherein the polypeptide is non-covalently associated with the peptidoglycan layer;
- (k) an *Alloiococcus otitidis* polypeptide having an RGD_X motif wherein X is not a proline residue;
- 25 (l) an *Alloiococcus otitidis* polypeptide predicted by BlastP as being involved in capsule biosynthesis and transport;
- (m) an *Alloiococcus otitidis* polypeptide identified by BlastP as being localized within the capsule loci of the *Alloiococcus otitidis* genome;
- 30 (n) an *Alloiococcus otitidis* polypeptide predicted by BlastP as being associated with sporulation;
- (o) an *Alloiococcus otitidis* polypeptide encoded by unique ORFs identified by BlastP analysis as having a BlastP 'E Value' of $> e^{-10}$;

- (p) an *Alloioococcus otitidis* polypeptide identified by Glimmer™ ORF finder program;
- (q) an *Alloioococcus otitidis* polypeptide identified by GeneMark™ ORF finder program;
- 5 (r) an *Alloioococcus otitidis* polypeptide identified by an ORF finder program that searches for an ATG, GTG or TTG Start codon between a Stop-Stop region; and
- (s) an *Alloioococcus otitidis* polypeptide identified by an ORF finder program that searches for a transmembrane domain between two Stop codons and
- 10 a Start codon immediately upstream of this transmembrane region.

8. The polynucleotide of claim 7, wherein the polynucleotide is a complement to a nucleotide sequence selected from one of the odd numbered sequences from SEQ ID NO: 1 to SEQ ID NO: 6649, a degenerate variant thereof, and a fragment thereof.

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9. The polynucleotide of claim 8, wherein the polynucleotide is selected from the group consisting of genomic DNA, cDNA and RNA.

20 10. The polynucleotide of claim 9, wherein the polynucleotide further comprises heterologous nucleotides.

11. The polynucleotide of claim 10, wherein the polynucleotide encodes a fusion polypeptide.

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12. The polynucleotide of claim 7 wherein the polynucleotide encodes a polypeptide, which is predicted by SignalP algorithm analysis as having met all four criteria set out in the SignalP algorithm for a polypeptide having a signal peptide, and which is predicted by HMM SignalP algorithm analysis as having a signal peptide, and the polynucleotide is selected from one of Seq. ID No. 89, Seq. ID No. 127, Seq. ID No. 131, Seq. ID No. 133, Seq. ID No. 161, Seq. ID No. 163, Seq. ID No. 213, Seq. ID No. 215, Seq. ID No. 225, Seq. ID No. 249, Seq. ID No. 251, Seq. ID No. 287, Seq. ID No. 289, Seq. ID No. 369, Seq. ID No. 371, Seq. ID No. 375, Seq.

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13. The polynucleotide of claim 7 wherein the polynucleotide encodes a polypeptide, which is predicted by SignalP algorithm analysis as having met three of the four criteria set out in the SignalP algorithm for a polypeptide having a signal peptide and which is predicted by HMM SignalP algorithm analysis as having a signal peptide, and the polynucleotide is selected from one of Seq. ID No. 7, Seq. ID No. 11, Seq. ID No. 23, Seq. ID No. 45, Seq. ID No. 47, Seq. ID No. 53, Seq. ID No. 59, Seq. ID No. 65, Seq. ID No. 67, Seq. ID No. 87, Seq. ID No. 91, Seq. ID No. 139, Seq. ID No. 151, Seq. ID No. 159, Seq. ID No. 165, Seq. ID No. 169, Seq. ID No. 185, Seq. ID No. 211, Seq. ID No. 217, Seq. ID No. 235, Seq. ID No. 237, Seq. ID No. 239, Seq. ID No. 271, Seq. ID No. 285, Seq. ID No. 291, Seq. ID No. 327, Seq. ID No. 349, Seq. ID No. 385, Seq. ID No. 387, Seq. ID No. 407,

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15 ID No. 6639, Seq. ID No. 6643, and Seq. ID No. 6645.

14. The polynucleotide of claim 7 wherein the polynucleotide encodes a polypeptide,
which is predicted by HMM Signal P algorithm analysis as having a signal
peptide, and the polynucleotide is selected from one of Seq. ID No. 3, Seq. ID
20 No. 7, Seq. ID No. 9, Seq. ID No. 19, Seq. ID No. 21, Seq. ID No. 31, Seq. ID No.
33, Seq. ID No. 45, Seq. ID No. 47, Seq. ID No. 49, Seq. ID No. 53, Seq. ID No.
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Seq. ID No. 6637, Seq. ID No. 6639, Seq. ID No. 6643, Seq. ID No. 6645, and Seq. ID No. 6649.

15. The polynucleotide of claim 7, wherein the polynucleotide encodes a polypeptide,
5 which is predicted by HMM Signal P algorithm analysis as being a non-secretory protein, and the polynucleotide is selected from one of Seq. ID No. 1, Seq. ID No. 5, Seq. ID No. 11, Seq. ID No. 13, Seq. ID No. 15, Seq. ID No. 17, Seq. ID No. 23, Seq. ID No. 25, Seq. ID No. 27, Seq. ID No. 29, Seq. ID No. 35, Seq. ID No. 37, Seq. ID No. 39, Seq. ID No. 41, Seq. ID No. 43, Seq. ID No. 51, Seq. ID No. 55, Seq. ID No. 57, Seq. ID No. 59, Seq. ID No. 61, Seq. ID No. 63, Seq. ID No. 69, Seq. ID No. 71, Seq. ID No. 73, Seq. ID No. 75, Seq. ID No. 77, Seq. ID No. 79, Seq. ID No. 81, Seq. ID No. 83, Seq. ID No. 89, Seq. ID No. 91, Seq. ID No. 93, Seq. ID No. 95, Seq. ID No. 97, Seq. ID No. 99, Seq. ID No. 101, Seq. ID No. 103, Seq. ID No. 107, Seq. ID No. 109, Seq. ID No. 113, Seq. ID No. 115, Seq. ID No. 117, Seq. ID No. 119, Seq. ID No. 121, Seq. ID No. 125, Seq. ID No. 127, Seq. ID No. 129, Seq. ID No. 135, Seq. ID No. 137, Seq. ID No. 139, Seq. ID No. 143, Seq. ID No. 145, Seq. ID No. 147, Seq. ID No. 149, Seq. ID No. 151, Seq. ID No. 153, Seq. ID No. 155, Seq. ID No. 157, Seq. ID No. 165, Seq. ID No. 167, Seq. ID No. 169, Seq. ID No. 173, Seq. ID No. 175, Seq. ID No. 177, Seq. ID No. 179, Seq. ID No. 181, Seq. ID No. 183, Seq. ID No. 185, Seq. ID No. 187, Seq. ID No. 189, Seq. ID No. 193, Seq. ID No. 195, Seq. ID No. 197, Seq. ID No. 199, Seq. ID No. 201, Seq. ID No. 203, Seq. ID No. 205, Seq. ID No. 207, Seq. ID No. 219, Seq. ID No. 221, Seq. ID No. 223, Seq. ID No. 227, Seq. ID No. 229, Seq. ID No. 231, Seq. ID No. 233, Seq. ID No. 239, Seq. ID No. 241, Seq. ID No. 243, Seq. ID No. 245, Seq. ID No. 247, Seq. ID No. 253, Seq. ID No. 261, Seq. ID No. 263, Seq. ID No. 265, Seq. ID No. 267, Seq. ID No. 269, Seq. ID No. 275, Seq. ID No. 279, Seq. ID No. 281, Seq. ID No. 283, Seq. ID No. 291, Seq. ID No. 293, Seq. ID No. 295, Seq. ID No. 297, Seq. ID No. 299, Seq. ID No. 301, Seq. ID No. 303, Seq. ID No. 305, Seq. ID No. 307, Seq. ID No. 309, Seq. ID No. 311, Seq. ID No. 313, Seq. ID No. 315, Seq. ID No. 317, Seq. ID No. 319, Seq. ID No. 321, Seq. ID No. 323, Seq. ID No. 325, Seq. ID No. 331, Seq. ID No. 333, Seq. ID No. 335, Seq. ID No. 337, Seq. ID No. 339, Seq. ID No. 341, Seq. ID No. 343, Seq. ID No. 345, Seq. ID No. 347, Seq. ID No. 349, Seq. ID No. 351, Seq. ID No. 353,

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16. The polynucleotide of claim 7, wherein the polynucleotide encoding a polypeptide is identified by Pfam analysis, and the polynucleotide is selected from one of Seq. ID No. 89, Seq. ID No. 145, Seq. ID No. 155, Seq. ID No. 167, Seq. ID No. 173, Seq. ID No. 191, Seq. ID No. 215, Seq. ID No. 219, Seq. ID No. 221, Seq. ID No. 223, Seq. ID No. 225, Seq. ID No. 233, Seq. ID No. 239, Seq. ID No. 251, Seq. ID No. 253, Seq. ID No. 271, Seq. ID No. 291, Seq. ID No. 331, Seq. ID No. 341, Seq. ID No. 345, Seq. ID No. 375, Seq. ID No. 501, Seq. ID No. 505, Seq. ID No. 511, Seq. ID No. 529, Seq. ID No. 567, Seq. ID No. 569, Seq. ID No. 575, Seq. ID No. 593, Seq. ID No. 595, Seq. ID No. 601, Seq. ID No. 637, Seq. ID No. 649,

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ID No. 6587, and Seq. ID No. 6591

17. The polynucleotide of claim 7, wherein the polynucleotide encoding a polypeptide
is identified by BlastP analysis, and the polynucleotide is selected from one of
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167, Seq. ID No. 171, Seq. ID No. 191, Seq. ID No. 215, Seq. ID No. 217, Seq.
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- 5 18. The polynucleotide of claim 7, wherein the polynucleotide has been identified using the proteomic methods used for studying surface exposed proteins of *Streptococcus pneumoniae* as encoding a polypeptide, and the polynucleotide is selected from one of Seq. ID No. 1, Seq. ID No. 5, Seq. ID No. 93, Seq. ID No. 95, Seq. ID No. 103, Seq. ID No. 107, Seq. ID No. 157, Seq. ID No. 223, Seq. ID No. 225, Seq. ID No. 233, Seq. ID No. 239, Seq. ID No. 253, Seq. ID No. 317, Seq. ID No. 321, Seq. ID No. 341, Seq. ID No. 345, Seq. ID No. 353, Seq. ID No. 361, Seq. ID No. 363, Seq. ID No. 365, Seq. ID No. 375, Seq. ID No. 379, Seq. ID No. 383, Seq. ID No. 389, Seq. ID No. 391, Seq. ID No. 397, Seq. ID No. 405, Seq. ID No. 409, Seq. ID No. 415, Seq. ID No. 423, Seq. ID No. 425, Seq. ID No. 427, Seq. ID No. 429, Seq. ID No. 435, Seq. ID No. 437, Seq. ID No. 439, Seq. ID No. 441, Seq. ID No. 443, Seq. ID No. 445, Seq. ID No. 447, Seq. ID No. 449, Seq. ID No. 461, Seq. ID No. 463, Seq. ID No. 465, Seq. ID No. 513, Seq. ID No. 543, Seq. ID No. 551, Seq. ID No. 553, Seq. ID No. 559, Seq. ID No. 595, Seq. ID No. 601, Seq. ID No. 637, Seq. ID No. 649, Seq. ID No. 657, Seq. ID No. 669, Seq. ID No. 675, Seq. ID No. 683, Seq. ID No. 753, Seq. ID No. 929, Seq. ID No. 969, Seq. ID No. 1041, Seq. ID No. 1043, Seq. ID No. 1085, Seq. ID No. 1089, Seq. ID No. 1093, Seq. ID No. 1097, Seq. ID No. 1099, Seq. ID No. 1101, Seq. ID No. 1175, Seq. ID No. 1205, Seq. ID No. 1237, Seq. ID No. 1459, Seq. ID No. 1495, Seq. ID No. 1497, Seq. ID No. 1503, Seq. ID No. 1517, Seq. ID No. 1527, Seq. ID No. 1531, Seq. ID No. 1539, Seq. ID No. 1543, Seq. ID No. 1549, Seq. ID No. 1573, Seq. ID No. 1657, Seq. ID No. 1709, Seq. ID No. 1767, Seq. ID No. 1785, Seq. ID No. 1821, Seq. ID No. 1889, Seq. ID No. 1925, Seq. ID No. 1969, Seq. ID No. 2003, Seq. ID No. 2047, Seq. ID No. 2075, Seq. ID No. 2089, Seq. ID No. 2093, Seq. ID No. 2117, Seq. ID No. 2137, Seq. ID No. 2143, Seq. ID No. 2205, Seq. ID No. 2235, Seq. ID No. 2257, Seq. ID No. 2301, Seq. ID No. 2363, Seq. ID No. 2423, Seq. ID No. 2445, Seq. ID No. 2451, Seq. ID No. 2481, Seq. ID No. 2495, Seq. ID No. 2505, Seq. ID No. 2577, Seq. ID No. 2587, Seq. ID No. 2613, Seq. ID No. 2633, Seq. ID No. 2651, Seq. ID No. 2665, Seq. ID No. 2669,

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4849, Seq. ID No. 4855, Seq. ID No. 4889, Seq. ID No. 4901, Seq. ID No. 4915,
Seq. ID No. 4917, Seq. ID No. 4931, Seq. ID No. 4935, Seq. ID No. 4977, Seq.
20 ID No. 5025, Seq. ID No. 5029, Seq. ID No. 5109, Seq. ID No. 5115, Seq. ID No.
5117, Seq. ID No. 5155, Seq. ID No. 5185, Seq. ID No. 5201, Seq. ID No. 5203,
Seq. ID No. 5219, Seq. ID No. 5261, Seq. ID No. 5289, Seq. ID No. 5295, Seq.
ID No. 5377, Seq. ID No. 5389, Seq. ID No. 5399, Seq. ID No. 5411, Seq. ID No.
5537, Seq. ID No. 5621, Seq. ID No. 5627, Seq. ID No. 5657, Seq. ID No. 5675,
25 Seq. ID No. 5717, Seq. ID No. 5777, Seq. ID No. 5859, Seq. ID No. 5901, Seq.
ID No. 5913, Seq. ID No. 5919, Seq. ID No. 5925, Seq. ID No. 5933, Seq. ID No.
6055, Seq. ID No. 6129, Seq. ID No. 6133, Seq. ID No. 6187, Seq. ID No. 6193,
Seq. ID No. 6219, Seq. ID No. 6271, Seq. ID No. 6277, Seq. ID No. 6369, Seq.
ID No. 6375, Seq. ID No. 6379, Seq. ID No. 6389, Seq. ID No. 6591, and Seq. ID
30 No. 6605.

19. The polynucleotide of claim 7, wherein the polypeptide encoded by the
polynucleotide was identified using HMM LPXTG motif finder as having a LPXTG

- motif and wherein the polypeptide is covalently attached to the peptidoglycan layer, and the polynucleotide is selected from one of Seq. ID No. 503, Seq. ID No. 505, Seq. ID No. 1315, Seq. ID No. 1317, Seq. ID No. 1363, Seq. ID No. 1365, Seq. ID No. 1367, Seq. ID No. 1369, Seq. ID No. 1559, Seq. ID No. 1561, Seq. ID No. 1581, Seq. ID No. 1739, Seq. ID No. 1741, Seq. ID No. 2811, Seq. ID No. 2813, Seq. ID No. 3619, Seq. ID No. 5587, Seq. ID No. 5589, Seq. ID No. 5591, Seq. ID No. 5781, Seq. ID No. 5783, and Seq. ID No. 6103.
20. The polynucleotide of claim Z, wherein the polynucleotide encodes a lipoprotein as predicted by HMM Lipo software program, and the polynucleotide is selected from one of Seq. ID No. 45, Seq. ID No. 47, Seq. ID No. 171, Seq. ID No. 225, Seq. ID No. 419, Seq. ID No. 513, Seq. ID No. 575, Seq. ID No. 591, Seq. ID No. 593, Seq. ID No. 657, Seq. ID No. 659, Seq. ID No. 669, Seq. ID No. 675, Seq. ID No. 745, Seq. ID No. 747, Seq. ID No. 935, Seq. ID No. 1045, Seq. ID No. 1075, Seq. ID No. 1137, Seq. ID No. 1173, Seq. ID No. 1191, Seq. ID No. 1193, Seq. ID No. 1195, Seq. ID No. 1563, Seq. ID No. 1661, Seq. ID No. 1663, Seq. ID No. 1665, Seq. ID No. 1791, Seq. ID No. 1797, Seq. ID No. 1917, Seq. ID No. 1969, Seq. ID No. 2115, Seq. ID No. 2159, Seq. ID No. 2429, Seq. ID No. 2527, Seq. ID No. 2699, Seq. ID No. 2815, Seq. ID No. 2875, Seq. ID No. 2975, Seq. ID No. 2977, Seq. ID No. 2991, Seq. ID No. 3043, Seq. ID No. 3323, Seq. ID No. 3337, Seq. ID No. 4133, Seq. ID No. 4137, Seq. ID No. 4481, Seq. ID No. 4705, Seq. ID No. 4827, Seq. ID No. 4869, Seq. ID No. 5115, Seq. ID No. 5377, Seq. ID No. 5379, Seq. ID No. 5491, Seq. ID No. 5509, Seq. ID No. 5513, Seq. ID No. 5525, Seq. ID No. 5529, Seq. ID No. 5531, Seq. ID No. 5889, Seq. ID No. 5909, Seq. ID No. 6025, Seq. ID No. 6027, Seq. ID No. 6087, Seq. ID No. 6089, Seq. ID No. 6325, Seq. ID No. 6327, Seq. ID No. 6415, Seq. ID No. 6637, Seq. ID No. 6639, and Seq. ID No. 6645.
- 21 The polynucleotide of claim 7, wherein the polypeptide encoded by the polynucleotide is predicted by HMM program to be non-covalently bound to the peptidoglycan layer, and the polynucleotide is selected from one of Seq. ID No. 3589, Seq. ID No. 3987, Seq. ID No. 5219, and Seq. ID No. 5337.

22. The polynucleotide of claim Z, wherein the polynucleotide encodes a polypeptide having a RGD_X motif wherein X is not a proline, and the polynucleotide is selected from one of Seq. ID No. 37, Seq. ID No. 99, Seq. ID No. 107, Seq. ID No. 109, Seq. ID No. 111, Seq. ID No. 351, Seq. ID No. 353, Seq. ID No. 465, Seq. ID No. 467, Seq. ID No. 469, Seq. ID No. 471, Seq. ID No. 683, Seq. ID No. 821, Seq. ID No. 823, Seq. ID No. 1021, Seq. ID No. 1023, Seq. ID No. 1157, Seq. ID No. 1159, Seq. ID No. 1233, Seq. ID No. 1333, Seq. ID No. 1335, Seq. ID No. 1449, Seq. ID No. 1559, Seq. ID No. 1561, Seq. ID No. 1563, Seq. ID No. 1625, Seq. ID No. 1777, Seq. ID No. 1827, Seq. ID No. 1829, Seq. ID No. 1871, Seq. ID No. 1925, Seq. ID No. 2135, Seq. ID No. 2145, Seq. ID No. 2173, Seq. ID No. 2175, Seq. ID No. 2177, Seq. ID No. 2179, Seq. ID No. 2259, Seq. ID No. 2317, Seq. ID No. 2319, Seq. ID No. 2321, Seq. ID No. 2323, Seq. ID No. 2325, Seq. ID No. 2327, Seq. ID No. 2329, Seq. ID No. 2401, Seq. ID No. 2671, Seq. ID No. 2863, Seq. ID No. 2869, Seq. ID No. 2919, Seq. ID No. 2921, Seq. ID No. 2993, Seq. ID No. 3087, Seq. ID No. 3137, Seq. ID No. 3279, Seq. ID No. 3281, Seq. ID No. 3283, Seq. ID No. 3333, Seq. ID No. 3335, Seq. ID No. 3497, Seq. ID No. 3499, Seq. ID No. 3501, Seq. ID No. 3533, Seq. ID No. 3671, Seq. ID No. 3673, Seq. ID No. 3675, Seq. ID No. 3837, Seq. ID No. 3839, Seq. ID No. 3841, Seq. ID No. 3843, Seq. ID No. 3929, Seq. ID No. 3961, Seq. ID No. 4037, Seq. ID No. 4193, Seq. ID No. 4239, Seq. ID No. 4327, Seq. ID No. 4329, Seq. ID No. 4333, Seq. ID No. 4393, Seq. ID No. 4463, Seq. ID No. 4465, Seq. ID No. 4467, Seq. ID No. 4597, Seq. ID No. 4629, Seq. ID No. 4631, Seq. ID No. 4675, Seq. ID No. 4677, Seq. ID No. 4679, Seq. ID No. 4689, Seq. ID No. 4691, Seq. ID No. 4693, Seq. ID No. 4781, Seq. ID No. 4799, Seq. ID No. 4801, Seq. ID No. 4803, Seq. ID No. 4861, Seq. ID No. 5009, Seq. ID No. 5143, Seq. ID No. 5145, Seq. ID No. 5179, Seq. ID No. 5181, Seq. ID No. 5183, Seq. ID No. 5249, Seq. ID No. 5251, Seq. ID No. 5253, Seq. ID No. 5259, Seq. ID No. 5261, Seq. ID No. 5293, Seq. ID No. 5295, Seq. ID No. 5297, Seq. ID No. 5299, Seq. ID No. 5307, Seq. ID No. 5309, Seq. ID No. 5411, Seq. ID No. 5535, Seq. ID No. 5537, Seq. ID No. 5745, Seq. ID No. 5821, Seq. ID No. 5823, Seq. ID No. 5825, Seq. ID No. 6029, Seq. ID No. 6171, Seq. ID No. 6307, Seq. ID No. 6309, and Seq. ID No. 6311.

23. The polynucleotide of claim 2, wherein the polynucleotide encodes a polypeptide that is predicted by BlastP analysis as being involved in capsule biosynthesis and transport, and the polynucleotide is selected from one of Seq. ID No. 49, Seq. ID No. 51, Seq. ID No. 53, Seq. ID No. 59, Seq. ID No. 195, Seq. ID No. 689, Seq. ID No. 703, Seq. ID No. 925, Seq. ID No. 1597, Seq. ID No. 1601, Seq. ID No. 1607, Seq. ID No. 1611, Seq. ID No. 1613, Seq. ID No. 1713, Seq. ID No. 2029, Seq. ID No. 2263, Seq. ID No. 2269, Seq. ID No. 2373, Seq. ID No. 2437, Seq. ID No. 2651, Seq. ID No. 2767, Seq. ID No. 2907, Seq. ID No. 3397, Seq. ID No. 3399, Seq. ID No. 3479, Seq. ID No. 3487, Seq. ID No. 3491, Seq. ID No. 3493, Seq. ID No. 3495, Seq. ID No. 3497, Seq. ID No. 3519, Seq. ID No. 3521, Seq. ID No. 3529, Seq. ID No. 3535, Seq. ID No. 3561, Seq. ID No. 3883, Seq. ID No. 3891, Seq. ID No. 3981, and Seq. ID No. 4087.

24. The polynucleotide of claim 7, wherein the polynucleotide encodes a polypeptide identified by BlastP analysis as being localized within the capsular loci of the *Alloiococcus otitidis* genome, and the polynucleotide is selected from one of Seq. ID No. 45, Seq. ID No. 47, Seq. ID No. 51, Seq. ID No. 53, Seq. ID No. 55, Seq. ID No. 57, Seq. ID No. 59, Seq. ID No. 683, Seq. ID No. 685, Seq. ID No. 687, Seq. ID No. 689, Seq. ID No. 691, Seq. ID No. 693, Seq. ID No. 695, Seq. ID No. 697, Seq. ID No. 699, Seq. ID No. 701, Seq. ID No. 703, Seq. ID No. 705, Seq. ID No. 707, Seq. ID No. 709, Seq. ID No. 711, Seq. ID No. 713, Seq. ID No. 715, Seq. ID No. 717, Seq. ID No. 719, Seq. ID No. 721, Seq. ID No. 723, Seq. ID No. 725, Seq. ID No. 727, Seq. ID No. 729, Seq. ID No. 731, Seq. ID No. 733, Seq. ID No. 735, Seq. ID No. 737, Seq. ID No. 739, Seq. ID No. 741, Seq. ID No. 743, Seq. ID No. 745, Seq. ID No. 747, Seq. ID No. 749, Seq. ID No. 751, Seq. ID No. 753, Seq. ID No. 3389, Seq. ID No. 3391, Seq. ID No. 3393, Seq. ID No. 3395, Seq. ID No. 3397, Seq. ID No. 3399, Seq. ID No. 3401, Seq. ID No. 3403, Seq. ID No. 3405, Seq. ID No. 3407, Seq. ID No. 3409, Seq. ID No. 3411, Seq. ID No. 3413, Seq. ID No. 3415, Seq. ID No. 3417, Seq. ID No. 3419, Seq. ID No. 3421, Seq. ID No. 3423, Seq. ID No. 3425, Seq. ID No. 3427, Seq. ID No. 3429, Seq. ID No. 3431, Seq. ID No. 3433, Seq. ID No. 3435, Seq. ID No. 3437, Seq. ID No. 3439, Seq. ID No. 3441, Seq. ID No. 3443, Seq. ID No. 3445, Seq. ID No. 3447, Seq. ID No. 3449, Seq. ID No. 3451, Seq. ID No. 3453, Seq. ID No. 3455, Seq.

ID No. 3457, Seq. ID No. 3459, Seq. ID No. 3461, Seq. ID No. 3463, Seq. ID No. 3465, Seq. ID No. 3467, Seq. ID No. 3469, Seq. ID No. 3471, Seq. ID No. 3473, Seq. ID No. 3475, Seq. ID No. 3477, Seq. ID No. 3479, Seq. ID No. 3481, Seq. ID No. 3483, Seq. ID No. 3485, Seq. ID No. 3487, Seq. ID No. 3489, Seq. ID No. 3491, Seq. ID No. 3493, Seq. ID No. 3495, Seq. ID No. 3497, Seq. ID No. 3499, Seq. ID No. 3501, Seq. ID No. 3503, Seq. ID No. 3505, Seq. ID No. 3507, Seq. ID No. 3509, Seq. ID No. 3511, Seq. ID No. 3513, Seq. ID No. 3515, Seq. ID No. 3517, Seq. ID No. 3519, Seq. ID No. 3521, Seq. ID No. 3523, Seq. ID No. 3525, Seq. ID No. 3527, Seq. ID No. 3529, Seq. ID No. 3531, Seq. ID No. 3533, Seq. ID No. 3535, Seq. ID No. 3537, Seq. ID No. 3539, Seq. ID No. 3541, Seq. ID No. 3543, Seq. ID No. 3545, Seq. ID No. 3547, Seq. ID No. 3549, Seq. ID No. 3551, Seq. ID No. 3553, Seq. ID No. 3555, Seq. ID No. 3557, Seq. ID No. 3559, and Seq. ID No. 3561.

25. The polynucleotide of claim 2, wherein the polynucleotide encodes a polypeptide identified by BlastP analysis as being associated with sporulation, and the polynucleotide is selected from one of Seq. ID No. 1137, Seq. ID No. 1455, Seq. ID No. 2137, Seq. ID No. 2141, Seq. ID No. 2165, Seq. ID No. 2179, Seq. ID No. 2301, Seq. ID No. 2753, Seq. ID No. 4211, Seq. ID No. 4251, Seq. ID No. 4327, Seq. ID No. 4569, Seq. ID No. 4719, and Seq. ID No. 4729.
26. The polynucleotide of claim 7, wherein the polynucleotide is a unique ORF identified by BlastP analysis as having a BlastP 'E' value of $>e^{-10}$, and the polynucleotide is selected from one of Seq. ID No. 7, Seq. ID No. 19, Seq. ID No. 21, Seq. ID No. 23, Seq. ID No. 31, Seq. ID No. 39, Seq. ID No. 65, Seq. ID No. 67, Seq. ID No. 69, Seq. ID No. 91, Seq. ID No. 99, Seq. ID No. 105, Seq. ID No. 113, Seq. ID No. 115, Seq. ID No. 123, Seq. ID No. 125, Seq. ID No. 127, Seq. ID No. 131, Seq. ID No. 133, Seq. ID No. 139, Seq. ID No. 151, Seq. ID No. 159, Seq. ID No. 161, Seq. ID No. 163, Seq. ID No. 165, Seq. ID No. 169, Seq. ID No. 185, Seq. ID No. 189, Seq. ID No. 193, Seq. ID No. 229, Seq. ID No. 231, Seq. ID No. 255, Seq. ID No. 257, Seq. ID No. 259, Seq. ID No. 275, Seq. ID No. 337, Seq. ID No. 339, Seq. ID No. 347, Seq. ID No. 349, Seq. ID No. 357, Seq. ID No. 359, Seq. ID No. 369, Seq. ID No. 371, Seq. ID No. 377, Seq. ID No. 385, Seq.

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20 ID No. 1977, Seq. ID No. 1981, Seq. ID No. 2005, Seq. ID No. 2007, Seq. ID No.
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27. The polynucleotide of claim 7, wherein the polypeptide encoded by the
5 polynucleotide is identified by GLIMMER™ ORF finder program, and the
polynucleotide is selected from one of Seq. ID No. 1, Seq. ID No. 5, Seq. ID No.
11, Seq. ID No. 13, Seq. ID No. 15, Seq. ID No. 17, Seq. ID No. 25, Seq. ID No.
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5 ID No. 4991, Seq. ID No. 4995, Seq. ID No. 4997, Seq. ID No. 5001, Seq. ID No. 5007, Seq. ID No. 5009, Seq. ID No. 5017, Seq. ID No. 5021, Seq. ID No. 5027, Seq. ID No. 5029, Seq. ID No. 5039, Seq. ID No. 5047, Seq. ID No. 5051, Seq. ID No. 5053, Seq. ID No. 5055, Seq. ID No. 5059, Seq. ID No. 5061, Seq. ID No. 5069, Seq. ID No. 5077, Seq. ID No. 5079, Seq. ID No. 5081, Seq. ID No. 5083, Seq. ID No. 5087, Seq. ID No. 5091, Seq. ID No. 5093, Seq. ID No. 5097, Seq. ID No. 5103, Seq. ID No. 5105, Seq. ID No. 5109, Seq. ID No. 5111, Seq. ID No. 5113, Seq. ID No. 5115, Seq. ID No. 5117, Seq. ID No. 5127, Seq. ID No. 5141, Seq. ID No. 5145, Seq. ID No. 5149, Seq. ID No. 5153, Seq. ID No. 5157, Seq. ID No. 5165, Seq. ID No. 5169, Seq. ID No. 5171, Seq. ID No. 5177, Seq. ID No. 5183, Seq. ID No. 5185, Seq. ID No. 5187, Seq. ID No. 5193, Seq. ID No. 5195, Seq. ID No. 5201, Seq. ID No. 5203, Seq. ID No. 5205, Seq. ID No. 5209, Seq. ID No. 5211, Seq. ID No. 5215, Seq. ID No. 5219, Seq. ID No. 5227, Seq. ID No. 5231, Seq. ID No. 5235, Seq. ID No. 5237, Seq. ID No. 5239, Seq. ID No. 5243, Seq. ID No. 5245, Seq. ID No. 5247, Seq. ID No. 5253, Seq. ID No. 5255, Seq. ID No. 5257, Seq. ID No. 5261, Seq. ID No. 5263, Seq. ID No. 5271, Seq. ID No. 5275, Seq. ID No. 5283, Seq. ID No. 5291, Seq. ID No. 5299, Seq. ID No. 5305, Seq. ID No. 5309, Seq. ID No. 5311, Seq. ID No. 5313, Seq. ID No. 5319, Seq. ID No. 5323, Seq. ID No. 5325, Seq. ID No. 5335, Seq. ID No. 5337, Seq. ID No. 5341, Seq. ID No. 5345, Seq. ID No. 5351, Seq. ID No. 5355, Seq. ID No. 5363, Seq. ID No. 5365, Seq. ID No. 5367, Seq. ID No. 5371, Seq. ID No. 5373, Seq. ID No. 5381, Seq. ID No. 5383, Seq. ID No. 5387, Seq. ID No. 5389, Seq. ID No. 5391, Seq. ID No. 5393, Seq. ID No. 5395, Seq. ID No. 5397, Seq. ID No. 5399, Seq. ID No. 5401, Seq. ID No. 5403, Seq. ID No. 5409, Seq. ID No. 5411, Seq. ID No. 5415, Seq. ID No. 5417, Seq. ID No. 5419, Seq. ID No. 5421, Seq. ID No. 5423, Seq. ID No. 5427, Seq. ID No. 5431, Seq. ID No. 5433, Seq. ID No. 5439, Seq. ID No. 5441, Seq. ID No. 5443, Seq. ID No. 5447, Seq. ID No. 5449, Seq. ID No. 5451, Seq. ID No. 5453, Seq. ID No. 5455, Seq. ID No. 5457, Seq. ID No. 5473, Seq. ID No. 5477, Seq. ID No. 5483, Seq. ID No. 5487, Seq. ID No. 5491, Seq. ID No. 5495, Seq. ID No. 5499, Seq. ID No. 5503, Seq. ID No. 5507, Seq. ID No. 5509, Seq. ID No. 5513, Seq. ID No. 5527, Seq. ID No. 5531, Seq. ID No. 5537, Seq. ID No. 5539, Seq. ID No. 5541, Seq. ID No. 5547, Seq. ID No. 5553, Seq. ID No. 5557, Seq. ID No. 5559, Seq. ID No. 5563, Seq. ID No. 5567, Seq.

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5 ID No. 6215, Seq. ID No. 6219, Seq. ID No. 6233, Seq. ID No. 6235, Seq. ID No. 6243, Seq. ID No. 6249, Seq. ID No. 6251, Seq. ID No. 6257, Seq. ID No. 6261, Seq. ID No. 6263, Seq. ID No. 6271, Seq. ID No. 6275, Seq. ID No. 6277, Seq. ID No. 6281, Seq. ID No. 6287, Seq. ID No. 6297, Seq. ID No. 6299, Seq. ID No. 6305, Seq. ID No. 6311, Seq. ID No. 6315, Seq. ID No. 6321, Seq. ID No. 6323, Seq. ID No. 6327, Seq. ID No. 6331, Seq. ID No. 6333, Seq. ID No. 6337, Seq. ID No. 6339, Seq. ID No. 6341, Seq. ID No. 6343, Seq. ID No. 6345, Seq. ID No. 6353, Seq. ID No. 6357, Seq. ID No. 6359, Seq. ID No. 6361, Seq. ID No. 6367, Seq. ID No. 6369, Seq. ID No. 6373, Seq. ID No. 6375, Seq. ID No. 6377, Seq. ID No. 6379, Seq. ID No. 6389, Seq. ID No. 6395, Seq. ID No. 6399, Seq. ID No. 6403, Seq. ID No. 6407, Seq. ID No. 6411, Seq. ID No. 6413, Seq. ID No. 6417, Seq. ID No. 6423, Seq. ID No. 6433, Seq. ID No. 6437, Seq. ID No. 6439, Seq. ID No. 6445, Seq. ID No. 6449, Seq. ID No. 6451, Seq. ID No. 6457, Seq. ID No. 6459, Seq. ID No. 6461, Seq. ID No. 6463, Seq. ID No. 6477, Seq. ID No. 6481, Seq. ID No. 6483, Seq. ID No. 6487, Seq. ID No. 6489, Seq. ID No. 6491, Seq. ID No. 6493, Seq. ID No. 6495, Seq. ID No. 6503, Seq. ID No. 6505, Seq. ID No. 6511, Seq. ID No. 6515, Seq. ID No. 6519, Seq. ID No. 6523, Seq. ID No. 6525, Seq. ID No. 6529, Seq. ID No. 6531, Seq. ID No. 6533, Seq. ID No. 6537, Seq. ID No. 6545, Seq. ID No. 6551, Seq. ID No. 6553, Seq. ID No. 6559, Seq. ID No. 6563, Seq. ID No. 6567, Seq. ID No. 6577, Seq. ID No. 6579, Seq. ID No. 6583, Seq. ID No. 6585, Seq. ID No. 6587, Seq. ID No. 6589, Seq. ID No. 6603, Seq. ID No. 6605, Seq. ID No. 6609, Seq. ID No. 6613, Seq. ID No. 6615, Seq. ID No. 6617, Seq. ID No. 6621, Seq. ID No. 6623, Seq. ID No. 6627, Seq. ID No. 6629, Seq. ID No. 6633, and Seq. ID No. 6639.

25 28. The polynucleotide of claim 7, wherein the polynucleotide encoded by the polynucleotide is identified by GeneMark™ ORF finder program, and the polynucleotide is selected from one of Seq. ID No. 1, Seq. ID No. 3, Seq. ID No. 11, Seq. ID No. 13, Seq. ID No. 15, Seq. ID No. 17, Seq. ID No. 25, Seq. ID No. 27, Seq. ID No. 29, Seq. ID No. 35, Seq. ID No. 37, Seq. ID No. 39, Seq. ID No. 41, Seq. ID No. 43, Seq. ID No. 45, Seq. ID No. 49, Seq. ID No. 53, Seq. ID No. 57, Seq. ID No. 61, Seq. ID No. 69, Seq. ID No. 71, Seq. ID No. 75, Seq. ID No. 81, Seq. ID No. 83, Seq. ID No. 89, Seq. ID No. 95, Seq. ID No. 101, Seq. ID No.

111, Seq. ID No. 119, Seq. ID No. 125, Seq. ID No. 129, Seq. ID No. 135, Seq.
ID No. 137, Seq. ID No. 141, Seq. ID No. 147, Seq. ID No. 151, Seq. ID No. 155,
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5 ID No. 207, Seq. ID No. 213, Seq. ID No. 219, Seq. ID No. 221, Seq. ID No. 225,
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10 303, Seq. ID No. 309, Seq. ID No. 311, Seq. ID No. 315, Seq. ID No. 319, Seq.
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15 Seq. ID No. 413, Seq. ID No. 417, Seq. ID No. 421, Seq. ID No. 423, Seq. ID No.
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29. The polynucleotide of claim 7, wherein the polynucleotide that encodes a polypeptide is identified using an ORF finder program that searches for an ATG, GTG or TTG Start codon between a Stop-Stop region, and the polynucleotide is selected from one of Seq. ID No. 1, Seq. ID No. 5, Seq. ID No. 11; Seq. ID No. 13, Seq. ID No. 15, Seq. ID No. 17, Seq. ID No. 19, Seq. ID No. 21, Seq. ID No. 23, Seq. ID No. 27, Seq. ID No. 29, Seq. ID No. 31, Seq. ID No. 35, Seq. ID No. 37, Seq. ID No. 41, Seq. ID No. 43, Seq. ID No. 45, Seq. ID No. 47, Seq. ID No. 49, Seq. ID No. 51, Seq. ID No. 53, Seq. ID No. 55, Seq. ID No. 57, Seq. ID No. 59, Seq. ID No. 65, Seq. ID No. 67, Seq. ID No. 75, Seq. ID No. 77, Seq. ID No. 79, Seq. ID No. 81, Seq. ID No. 83, Seq. ID No. 89, Seq. ID No. 91, Seq. ID No. 93, Seq. ID No. 97, Seq. ID No. 99, Seq. ID No. 103, Seq. ID No. 105, Seq. ID No. 107, Seq. ID No. 109, Seq. ID No. 111, Seq. ID No. 113, Seq. ID No. 115, Seq. ID No. 117, Seq. ID No. 119, Seq. ID No. 121, Seq. ID No. 127, Seq. ID No. 129, Seq. ID No. 131, Seq. ID No. 133, Seq. ID No. 135, Seq. ID No. 137, Seq. ID No. 139, Seq. ID No. 143, Seq. ID No. 145, Seq. ID No. 147, Seq. ID No. 149, Seq. ID No. 153, Seq. ID No. 155, Seq. ID No. 157, Seq. ID No. 159, Seq. ID No. 161, Seq. ID No. 163, Seq. ID No. 165, Seq. ID No. 167, Seq. ID No. 169, Seq.

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25 Seq. ID No. 6637, Seq. ID No. 6639, Seq. ID No. 6643, Seq. ID No. 6645, and
Seq. ID No. 6649.

30. The polynucleotide of claim 7 wherein the polynucleotide encodes a polypeptide
that is identified by an ORF finder program, which searches for a transmembrane
30 domain between two Stop codons and a Start codon immediately upstream of
this transmembrane region, and the polynucleotide is selected from one of Seq.
ID No. 7, Seq. ID No. 9, Seq. ID No. 33, Seq. ID No. 47, Seq. ID No. 67, Seq. ID
No. 85, Seq. ID No. 87, Seq. ID No. 123, Seq. ID No. 133, Seq. ID No. 141, Seq.

5 ID No. 159, Seq. ID No. 163, Seq. ID No. 191, Seq. ID No. 209, Seq. ID No. 211,
Seq. ID No. 215, Seq. ID No. 217, Seq. ID No. 225, Seq. ID No. 235, Seq. ID No.
237, Seq. ID No. 249, Seq. ID No. 251, Seq. ID No. 255, Seq. ID No. 271, Seq.
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10 Seq. ID No. 329, Seq. ID No. 373, Seq. ID No. 375, Seq. ID No. 419, Seq. ID No.
487, Seq. ID No. 497, Seq. ID No. 499, Seq. ID No. 503, Seq. ID No. 505, Seq.
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31. An isolated polynucleotide of an *Alloiococcus otitidis* genomic sequence, wherein the polynucleotide comprises a nucleotide sequence having at least about 70% identity to a nucleotide sequence contained within SEQ ID NO: 6651, a complement thereof, a degenerate variant thereof, and a fragment thereof.

32. An isolated polypeptide encoded by a polynucleotide comprising a nucleotide sequence having at least about 70% identity to a nucleotide sequence selected from one of odd numbered sequences from SEQ ID NO: 1 to SEQ ID NO: 6649, a degenerate variant thereof, and a fragment thereof.

33. The polypeptide of claim 32, wherein the polypeptide comprises an amino acid sequence having at least about 70% identity to an amino acid sequence chosen from one of the even-numbered sequences from SEQ ID NO: 2 to SEQ ID NO: 6650, a biological equivalent thereof, and a fragment thereof.

34. The polypeptide of claim 32, wherein the polypeptide is a fusion polypeptide.

35. The polypeptide of claim 32, which immunoreacts with seropositive serum of an individual infected with *Alloiococcus otitidis*.

36. The polypeptide of claim 32, further defined as:

- (a) an *Alloiococcus otitidis* polypeptide predicted by SignalP algorithm analysis as having met all four criteria set out in the SignalP algorithm for a polypeptide having a signal peptide and predicted by HMM Signal P algorithm analysis as having a signal peptide;

- (b) an *Alloiococcus otitidis* polypeptide predicted by SignalP algorithm analysis as having met three of the four criteria set out in the SignalP algorithm for a polypeptide having a signal peptide and predicted by HMM SignalP algorithm analysis as having a signal peptide;
- 5 (c) an *Alloiococcus otitidis* polypeptide predicted by HMM SignalP algorithm analysis as having a signal peptide;
- (d) an *Alloiococcus otitidis* polypeptide predicted by HMM SignalP algorithm analysis as being a non-secretory protein;
- (e) an *Alloiococcus otitidis* polypeptide identified by BlastP analysis;
- 10 (f) an *Alloiococcus otitidis* polypeptide identified by Pfam analysis;
- (g) an *Alloiococcus otitidis* polypeptide identified using proteomics methodology as sharing homology with surface exposed proteins of *Streptococcus pneumoniae*;
- (h) an *Alloiococcus otitidis* lipoprotein;
- 15 (i) an *Alloiococcus otitidis* polypeptide having a LPXTG motif, wherein the polypeptide is covalently attached to the peptidoglycan layer;
- (j) an *Alloiococcus otitidis* polypeptide, wherein the polypeptide is non-covalently associated with the peptidoglycan layer;
- (k) an *Alloiococcus otitidis* polypeptide having an RGD_X motif wherein X is not a proline residue;
- 20 (l) an *Alloiococcus otitidis* polypeptide predicted by BlastP as being involved in capsule biosynthesis and transport;
- (m) an *Alloiococcus otitidis* polypeptide identified by BlastP as being localized within the capsule loci of the *Alloiococcus otitidis* genome;
- 25 (n) an *Alloiococcus otitidis* polypeptide predicted by BlastP as being associated with sporulation;
- (o) an *Alloiococcus otitidis* polypeptide encoded by unique ORFs identified by BlastP analysis as having a BlastP 'E Value' of $> e^{-10}$;
- (p) an *Alloiococcus otitidis* polypeptide identified by Glimmer™ ORF finder program;
- 30 (q) an *Alloiococcus otitidis* polypeptide identified by GeneMark™ ORF finder program;

- (r) an *Alloiococcus otitidis* polypeptide identified by an ORF finder program that searches for an ATG, GTG or TTG Start codon between a Stop-Stop region; and
- (s) an *Alloiococcus otitidis* polypeptide identified by an ORF finder program that searches for a transmembrane domain between two Stop codon and a Start codon immediately upstream of this transmembrane region.

37. The *Alloiococcus otitidis* polypeptide of claim 36, wherein the polypeptide is predicted by SignalP algorithm analysis as having met all four criteria set out in the SignalP algorithm for a polypeptide having a signal peptide and predicted by HMM Signal P algorithm analysis as having a signal peptide; and is selected from one of Seq. ID No. 90, Seq. ID No. 128, Seq. ID No. 132, Seq. ID No. 134, Seq. ID No. 162, Seq. ID No. 164, Seq. ID No. 214, Seq. ID No. 216, Seq. ID No. 226, Seq. ID No. 250, Seq. ID No. 252, Seq. ID No. 288, Seq. ID No. 290, Seq. ID No. 370, Seq. ID No. 372, Seq. ID No. 376, Seq. ID No. 378, Seq. ID No. 498, Seq. ID No. 504, Seq. ID No. 506, Seq. ID No. 528, Seq. ID No. 550, Seq. ID No. 576, Seq. ID No. 618, Seq. ID No. 658, Seq. ID No. 660, Seq. ID No. 662, Seq. ID No. 676, Seq. ID No. 716, Seq. ID No. 718, Seq. ID No. 746, Seq. ID No. 748, Seq. ID No. 756, Seq. ID No. 758, Seq. ID No. 760, Seq. ID No. 762, Seq. ID No. 774, Seq. ID No. 808, Seq. ID No. 968, Seq. ID No. 974, Seq. ID No. 976, Seq. ID No. 1014, Seq. ID No. 1026, Seq. ID No. 1028, Seq. ID No. 1040, Seq. ID No. 1076, Seq. ID No. 1090, Seq. ID No. 1196, Seq. ID No. 1198, Seq. ID No. 1208, Seq. ID No. 1240, Seq. ID No. 1244, Seq. ID No. 1246, Seq. ID No. 1270, Seq. ID No. 1316, Seq. ID No. 1318, Seq. ID No. 1332, Seq. ID No. 1366, Seq. ID No. 1368, Seq. ID No. 1370, Seq. ID No. 1446, Seq. ID No. 1448, Seq. ID No. 1514, Seq. ID No. 1518, Seq. ID No. 1546, Seq. ID No. 1550, Seq. ID No. 1562, Seq. ID No. 1570, Seq. ID No. 1572, Seq. ID No. 1586, Seq. ID No. 1644, Seq. ID No. 1654, Seq. ID No. 1662, Seq. ID No. 1664, Seq. ID No. 1708, Seq. ID No. 1734, Seq. ID No. 1738, Seq. ID No. 1756, Seq. ID No. 1766, Seq. ID No. 1768, Seq. ID No. 1776, Seq. ID No. 1792, Seq. ID No. 1806, Seq. ID No. 1876, Seq. ID No. 1970, Seq. ID No. 1982, Seq. ID No. 2054, Seq. ID No. 2056, Seq. ID No. 2088, Seq. ID No. 2090, Seq. ID No. 2092, Seq. ID No. 2106, Seq. ID No. 2116, Seq. ID No. 2150, Seq. ID No. 2152, Seq. ID No. 2160, Seq. ID No. 2178, Seq. ID No. 2278,

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- 5 38. The *Alloiococcus otitidis* polypeptide of claim 36, wherein the polypeptide is predicted by SignalP algorithm analysis as having met three of the four criteria set out in the SignalP algorithm for a polypeptide having a signal peptide and predicted by HMM SignalP algorithm analysis as having a signal peptide; and is selected from one of Seq. ID No. 8, Seq. ID No. 12, Seq. ID No. 24, Seq. ID No. 10 46, Seq. ID No. 48, Seq. ID No. 54, Seq. ID No. 60, Seq. ID No. 66, Seq. ID No. 68, Seq. ID No. 88, Seq. ID No. 92, Seq. ID No. 140, Seq. ID No. 152, Seq. ID No. 160, Seq. ID No. 166, Seq. ID No. 170, Seq. ID No. 186, Seq. ID No. 212, Seq. ID No. 218, Seq. ID No. 236, Seq. ID No. 238, Seq. ID No. 240, Seq. ID No. 272, Seq. ID No. 286, Seq. ID No. 292, Seq. ID No. 328, Seq. ID No. 350, Seq. ID No. 386, Seq. ID No. 388, Seq. ID No. 408, Seq. ID No. 428, Seq. ID No. 432, 15 Seq. ID No. 456, Seq. ID No. 458, Seq. ID No. 496, Seq. ID No. 500, Seq. ID No. 512, Seq. ID No. 514, Seq. ID No. 516, Seq. ID No. 526, Seq. ID No. 546, Seq. ID No. 548, Seq. ID No. 558, Seq. ID No. 570, Seq. ID No. 590, Seq. ID No. 592, Seq. ID No. 594, Seq. ID No. 596, Seq. ID No. 610, Seq. ID No. 638, Seq. ID No. 20 640, Seq. ID No. 642, Seq. ID No. 654, Seq. ID No. 670, Seq. ID No. 680, Seq. ID No. 720, Seq. ID No. 724, Seq. ID No. 740, Seq. ID No. 750, Seq. ID No. 752, Seq. ID No. 764, Seq. ID No. 766, Seq. ID No. 770, Seq. ID No. 778, Seq. ID No. 780, Seq. ID No. 782, Seq. ID No. 820, Seq. ID No. 896, Seq. ID No. 904, Seq. ID No. 906, Seq. ID No. 910, Seq. ID No. 936, Seq. ID No. 938, Seq. ID No. 952, 25 Seq. ID No. 956, Seq. ID No. 980, Seq. ID No. 982, Seq. ID No. 984, Seq. ID No. 986, Seq. ID No. 1006, Seq. ID No. 1008, Seq. ID No. 1010, Seq. ID No. 1016, Seq. ID No. 1020, Seq. ID No. 1030, Seq. ID No. 1032, Seq. ID No. 1048, Seq. ID No. 1092, Seq. ID No. 1112, Seq. ID No. 1138, Seq. ID No. 1152, Seq. ID No. 1154, Seq. ID No. 1170, Seq. ID No. 1174, Seq. ID No. 1184, Seq. ID No. 1192, 30 Seq. ID No. 1194, Seq. ID No. 1214, Seq. ID No. 1224, Seq. ID No. 1230, Seq. ID No. 1248, Seq. ID No. 1260, Seq. ID No. 1284, Seq. ID No. 1308, Seq. ID No. 1320, Seq. ID No. 1322, Seq. ID No. 1328, Seq. ID No. 1342, Seq. ID No. 1344, Seq. ID No. 1348, Seq. ID No. 1390, Seq. ID No. 1402, Seq. ID No. 1430, Seq.

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30 and Seq. ID No. 6646.

39. The *Alloiococcus otitidis* polypeptide of claim 36, wherein the polypeptide is predicted by HMM SignalP algorithm analysis as having a signal peptide, and is selected from one of Seq. ID No. 4, Seq. ID No. 8, Seq. ID No. 10, Seq. ID No. 20, Seq. ID No. 22, Seq. ID No. 32, Seq. ID No. 34, Seq. ID No. 46, Seq. ID No. 48, Seq. ID No. 50, Seq. ID No. 54, Seq. ID No. 66, Seq. ID No. 68, Seq. ID No. 86, Seq. ID No. 88, Seq. ID No. 106, Seq. ID No. 112, Seq. ID No. 124, Seq. ID No. 132, Seq. ID No. 134, Seq. ID No. 142, Seq. ID No. 160, Seq. ID No. 162, Seq. ID No. 164, Seq. ID No. 172, Seq. ID No. 192, Seq. ID No. 210, Seq. ID No. 212, Seq. ID No. 214, Seq. ID No. 216, Seq. ID No. 218, Seq. ID No. 226, Seq. ID No. 236, Seq. ID No. 238, Seq. ID No. 250, Seq. ID No. 252, Seq. ID No. 256, Seq. ID No. 258, Seq. ID No. 260, Seq. ID No. 272, Seq. ID No. 274, Seq. ID No. 278, Seq. ID No. 286, Seq. ID No. 288, Seq. ID No. 290, Seq. ID No. 328, Seq. ID No. 330, Seq. ID No. 358, Seq. ID No. 360, Seq. ID No. 374, Seq. ID No. 376, Seq. ID No. 394, Seq. ID No. 402, Seq. ID No. 404, Seq. ID No. 456, Seq. ID No. 458, Seq. ID No. 478, Seq. ID No. 488, Seq. ID No. 490, Seq. ID No. 492, Seq. ID No. 494, Seq. ID No. 496, Seq. ID No. 498, Seq. ID No. 500, Seq. ID No. 504, Seq. ID No. 506, Seq. ID No. 510, Seq. ID No. 512, Seq. ID No. 514, Seq. ID No. 516, Seq. ID No. 526, Seq. ID No. 528, Seq. ID No. 546, Seq. ID No. 548, Seq. ID No. 550, Seq. ID No. 558, Seq. ID No. 568, Seq. ID No. 570, Seq. ID No. 576, Seq. ID No. 578, Seq. ID No. 580, Seq. ID No. 592, Seq. ID No. 594, Seq. ID No. 600, Seq. ID No. 618, Seq. ID No. 638, Seq. ID No. 640, Seq. ID No. 642, Seq. ID No. 644, Seq. ID No. 646, Seq. ID No. 648, Seq. ID No. 654, Seq. ID No. 656, Seq. ID No. 658, Seq. ID No. 660, Seq. ID No. 662, Seq. ID No. 668, Seq. ID No. 670, Seq. ID No. 676, Seq. ID No. 678, Seq. ID No. 680, Seq. ID No. 716, Seq. ID No. 718, Seq. ID No. 720, Seq. ID No. 722, Seq. ID No. 724, Seq. ID No. 726, Seq. ID No. 746, Seq. ID No. 748, Seq. ID No. 750, Seq. ID No. 752, Seq. ID No. 756, Seq. ID No. 758, Seq. ID No. 760, Seq. ID No. 762, Seq. ID No. 764, Seq. ID No. 766, Seq. ID No. 770, Seq. ID No. 778, Seq. ID No. 780, Seq. ID No. 782, Seq. ID No. 808, Seq. ID No. 810, Seq. ID No. 820, Seq. ID No. 826, Seq. ID No. 864, Seq. ID No. 894, Seq. ID No. 902, Seq. ID No. 936, Seq. ID No. 938, Seq. ID No. 942, Seq. ID No. 944, Seq. ID No. 956, Seq. ID No. 958, Seq. ID No. 968, Seq. ID No. 980, Seq. ID No. 982, Seq. ID No. 984, Seq. ID No. 986, Seq. ID No. 1002, Seq. ID No. 1004, Seq. ID No. 1006, Seq. ID No. 1008, Seq. ID No. 1010,

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40. The *Alloiococcus otitidis* polypeptide of claim 36, wherein the polypeptide is predicted by HMM SignalP algorithm analysis as being a non-secretory protein, and is selected from one of Seq. ID No. 2, Seq. ID No. 6, Seq. ID No. 12, Seq. ID No. 14, Seq. ID No. 16, Seq. ID No. 18, Seq. ID No. 24, Seq. ID No. 26, Seq. ID No. 28, Seq. ID No. 30, Seq. ID No. 36, Seq. ID No. 38, Seq. ID No. 40, Seq. ID No. 42, Seq. ID No. 44, Seq. ID No. 52, Seq. ID No. 56, Seq. ID No. 58, Seq. ID No. 60, Seq. ID No. 62, Seq. ID No. 64, Seq. ID No. 70, Seq. ID No. 72, Seq. ID No. 74, Seq. ID No. 76, Seq. ID No. 78, Seq. ID No. 80, Seq. ID No. 82, Seq. ID No. 84, Seq. ID No. 90, Seq. ID No. 92, Seq. ID No. 94, Seq. ID No. 96, Seq. ID No. 98, Seq. ID No. 100, Seq. ID No. 102, Seq. ID No. 104, Seq. ID No. 108, Seq. ID No. 110, Seq. ID No. 114, Seq. ID No. 116, Seq. ID No. 118, Seq. ID No. 120, Seq. ID No. 122, Seq. ID No. 126, Seq. ID No. 128, Seq. ID No. 130, Seq. ID No. 136, Seq. ID No. 138, Seq. ID No. 140, Seq. ID No. 144, Seq. ID No. 146, Seq. ID No. 148, Seq. ID No. 150, Seq. ID No. 152, Seq. ID No. 154, Seq. ID No. 156, Seq. ID No. 158, Seq. ID No. 166, Seq. ID No. 168, Seq. ID No. 170, Seq.

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6630, Seq. ID No. 6634, Seq. ID No. 6636, Seq. ID No. 6642, and Seq. ID No.
6648.

41. The *Alloiococcus otitidis* polypeptide of claim 36, wherein the polypeptide is
identified by BlastP analysis, and is selected from one of Seq. ID No. 10, Seq. ID
No. 18, Seq. ID No. 46, Seq. ID No. 50, Seq. ID No. 54, Seq. ID No. 60, Seq. ID
No. 90, Seq. ID No. 146, Seq. ID No. 158, Seq. ID No. 168, Seq. ID No. 172,
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ID No. 330, Seq. ID No. 344, Seq. ID No. 346, Seq. ID No. 376, Seq. ID No. 502,
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1966, Seq. ID No. 1972, Seq. ID No. 2000, Seq. ID No. 2048, Seq. ID No. 2056,
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5 Seq. ID No. 2704, Seq. ID No. 2710, Seq. ID No. 2716, Seq. ID No. 2752, Seq.
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2804, Seq. ID No. 2868, Seq. ID No. 2872, Seq. ID No. 2908, Seq. ID No. 2920,
Seq. ID No. 2922, Seq. ID No. 2924, Seq. ID No. 2928, Seq. ID No. 2934, Seq.
ID No. 2958, Seq. ID No. 2980, Seq. ID No. 3000, Seq. ID No. 3006, Seq. ID No.
10 3020, Seq. ID No. 3032, Seq. ID No. 3036, Seq. ID No. 3056, Seq. ID No. 3068,
Seq. ID No. 3086, Seq. ID No. 3166, Seq. ID No. 3184, Seq. ID No. 3190, Seq.
ID No. 3198, Seq. ID No. 3212, Seq. ID No. 3252, Seq. ID No. 3258, Seq. ID No.
3260, Seq. ID No. 3298, Seq. ID No. 3320, Seq. ID No. 3324, Seq. ID No. 3336,
Seq. ID No. 3338, Seq. ID No. 3356, Seq. ID No. 3360, Seq. ID No. 3378, Seq.
15 ID No. 3398, Seq. ID No. 3406, Seq. ID No. 3416, Seq. ID No. 3426, Seq. ID No.
3428, Seq. ID No. 3462, Seq. ID No. 3464, Seq. ID No. 3488, Seq. ID No. 3494,
Seq. ID No. 3498, Seq. ID No. 3508, Seq. ID No. 3520, Seq. ID No. 3522, Seq.
ID No. 3530, Seq. ID No. 3536, Seq. ID No. 3630, Seq. ID No. 3636, Seq. ID No.
3728, Seq. ID No. 3760, Seq. ID No. 3772, Seq. ID No. 3794, Seq. ID No. 3840,
20 Seq. ID No. 3852, Seq. ID No. 3864, Seq. ID No. 3866, Seq. ID No. 3884, Seq.
ID No. 3892, Seq. ID No. 3914, Seq. ID No. 3926, Seq. ID No. 3930, Seq. ID No.
3976, Seq. ID No. 3982, Seq. ID No. 4028, Seq. ID No. 4040, Seq. ID No. 4062,
Seq. ID No. 4074, Seq. ID No. 4082, Seq. ID No. 4104, Seq. ID No. 4112, Seq.
ID No. 4138, Seq. ID No. 4226, Seq. ID No. 4248, Seq. ID No. 4344, Seq. ID No.
25 4380, Seq. ID No. 4390, Seq. ID No. 4470, Seq. ID No. 4474, Seq. ID No. 4482,
Seq. ID No. 4486, Seq. ID No. 4494, Seq. ID No. 4530, Seq. ID No. 4644, Seq.
ID No. 4706, Seq. ID No. 4714, Seq. ID No. 4718, Seq. ID No. 4814, Seq. ID No.
4816, Seq. ID No. 4826, Seq. ID No. 4828, Seq. ID No. 4834, Seq. ID No. 4838,
Seq. ID No. 4852, Seq. ID No. 4864, Seq. ID No. 4876, Seq. ID No. 4880, Seq.
30 ID No. 4894, Seq. ID No. 4902, Seq. ID No. 4920, Seq. ID No. 4932, Seq. ID No.
4960, Seq. ID No. 4964, Seq. ID No. 4986, Seq. ID No. 5114, Seq. ID No. 5116,
Seq. ID No. 5118, Seq. ID No. 5126, Seq. ID No. 5142, Seq. ID No. 5184, Seq.
ID No. 5202, Seq. ID No. 5206, Seq. ID No. 5214, Seq. ID No. 5220, Seq. ID No.

5280, Seq. ID No. 5286, Seq. ID No. 5332, Seq. ID No. 5382, Seq. ID No. 5390,
Seq. ID No. 5406, Seq. ID No. 5412, Seq. ID No. 5420, Seq. ID No. 5434, Seq.
ID No. 5464, Seq. ID No. 5478, Seq. ID No. 5492, Seq. ID No. 5510, Seq. ID No.
5514, Seq. ID No. 5526, Seq. ID No. 5530, Seq. ID No. 5538, Seq. ID No. 5568,
5 Seq. ID No. 5600, Seq. ID No. 5622, Seq. ID No. 5638, Seq. ID No. 5700, Seq.
ID No. 5724, Seq. ID No. 5734, Seq. ID No. 5762, Seq. ID No. 5792, Seq. ID No.
5896, Seq. ID No. 5902, Seq. ID No. 5904, Seq. ID No. 5910, Seq. ID No. 5914,
Seq. ID No. 5920, Seq. ID No. 5930, Seq. ID No. 5940, Seq. ID No. 6002, Seq.
ID No. 6044, Seq. ID No. 6054, Seq. ID No. 6058, Seq. ID No. 6090, Seq. ID No.
10 6096, Seq. ID No. 6104, Seq. ID No. 6112, Seq. ID No. 6118, Seq. ID No. 6166,
Seq. ID No. 6170, Seq. ID No. 6186, Seq. ID No. 6192, Seq. ID No. 6210, Seq.
ID No. 6230, Seq. ID No. 6258, Seq. ID No. 6264, Seq. ID No. 6272, Seq. ID No.
6276, Seq. ID No. 6290, Seq. ID No. 6304, Seq. ID No. 6366, Seq. ID No. 6370,
Seq. ID No. 6384, and Seq. ID No. 6416.

- 15 42. The *Alloiococcus otitidis* polypeptide of claim 36, wherein the polypeptide is
identified by Pfam analysis, and is selected from one of Seq. ID No. 90, Seq. ID
No. 146, Seq. ID No. 156, Seq. ID No. 168, Seq. ID No. 174, Seq. ID No. 192,
Seq. ID No. 216, Seq. ID No. 220, Seq. ID No. 222, Seq. ID No. 224, Seq. ID No.
20 226, Seq. ID No. 234, Seq. ID No. 240, Seq. ID No. 252, Seq. ID No. 254, Seq.
ID No. 272, Seq. ID No. 292, Seq. ID No. 332, Seq. ID No. 342, Seq. ID No. 346,
Seq. ID No. 376, Seq. ID No. 502, Seq. ID No. 506, Seq. ID No. 512, Seq. ID No.
530, Seq. ID No. 568, Seq. ID No. 570, Seq. ID No. 576, Seq. ID No. 594, Seq.
ID No. 596, Seq. ID No. 602, Seq. ID No. 638, Seq. ID No. 650, Seq. ID No. 662,
25 Seq. ID No. 670, Seq. ID No. 676, Seq. ID No. 682, Seq. ID No. 684, Seq. ID No.
730, Seq. ID No. 754, Seq. ID No. 780, Seq. ID No. 828, Seq. ID No. 840, Seq.
ID No. 896, Seq. ID No. 940, Seq. ID No. 970, Seq. ID No. 986, Seq. ID No.
1016, Seq. ID No. 1040, Seq. ID No. 1076, Seq. ID No. 1138, Seq. ID No. 1156,
Seq. ID No. 1164, Seq. ID No. 1176, Seq. ID No. 1224, Seq. ID No. 1232, Seq.
30 ID No. 1238, Seq. ID No. 1242, Seq. ID No. 1262, Seq. ID No. 1332, Seq. ID No.
1340, Seq. ID No. 1370, Seq. ID No. 1478, Seq. ID No. 1518, Seq. ID No. 1532,
Seq. ID No. 1540, Seq. ID No. 1550, Seq. ID No. 1564, Seq. ID No. 1568, Seq.
ID No. 1572, Seq. ID No. 1574, Seq. ID No. 1590, Seq. ID No. 1596, Seq. ID No.

1648, Seq. ID No. 1658, Seq. ID No. 1772, Seq. ID No. 1786, Seq. ID No. 1790,
Seq. ID No. 1820, Seq. ID No. 1822, Seq. ID No. 1970, Seq. ID No. 2016, Seq.
ID No. 2048, Seq. ID No. 2088, Seq. ID No. 2090, Seq. ID No. 2094, Seq. ID No.
2116, Seq. ID No. 2118, Seq. ID No. 2128, Seq. ID No. 2142, Seq. ID No. 2180,
5 Seq. ID No. 2208, Seq. ID No. 2224, Seq. ID No. 2254, Seq. ID No. 2276, Seq.
ID No. 2302, Seq. ID No. 2316, Seq. ID No. 2330, Seq. ID No. 2344, Seq. ID No.
2350, Seq. ID No. 2364, Seq. ID No. 2382, Seq. ID No. 2392, Seq. ID No. 2418,
Seq. ID No. 2422, Seq. ID No. 2424, Seq. ID No. 2430, Seq. ID No. 2482, Seq.
ID No. 2488, Seq. ID No. 2490, Seq. ID No. 2492, Seq. ID No. 2510, Seq. ID No.
10 2520, Seq. ID No. 2526, Seq. ID No. 2548, Seq. ID No. 2554, Seq. ID No. 2564,
Seq. ID No. 2588, Seq. ID No. 2600, Seq. ID No. 2608, Seq. ID No. 2614, Seq.
ID No. 2652, Seq. ID No. 2676, Seq. ID No. 2682, Seq. ID No. 2688, Seq. ID No.
2694, Seq. ID No. 2700, Seq. ID No. 2704, Seq. ID No. 2710, Seq. ID No. 2712,
Seq. ID No. 2728, Seq. ID No. 2754, Seq. ID No. 2820, Seq. ID No. 2822, Seq.
15 ID No. 2824, Seq. ID No. 2868, Seq. ID No. 2872, Seq. ID No. 2908, Seq. ID No.
2920, Seq. ID No. 2958, Seq. ID No. 2972, Seq. ID No. 2980, Seq. ID No. 3000,
Seq. ID No. 3006, Seq. ID No. 3020, Seq. ID No. 3036, Seq. ID No. 3066, Seq.
ID No. 3086, Seq. ID No. 3150, Seq. ID No. 3166, Seq. ID No. 3184, Seq. ID No.
3204, Seq. ID No. 3212, Seq. ID No. 3252, Seq. ID No. 3260, Seq. ID No. 3320,
20 Seq. ID No. 3324, Seq. ID No. 3336, Seq. ID No. 3338, Seq. ID No. 3348, Seq.
ID No. 3360, Seq. ID No. 3378, Seq. ID No. 3380, Seq. ID No. 3400, Seq. ID No.
3426, Seq. ID No. 3484, Seq. ID No. 3496, Seq. ID No. 3498, Seq. ID No. 3520,
Seq. ID No. 3530, Seq. ID No. 3600, Seq. ID No. 3612, Seq. ID No. 3616, Seq.
ID No. 3620, Seq. ID No. 3664, Seq. ID No. 3740, Seq. ID No. 3760, Seq. ID No.
25 3772, Seq. ID No. 3798, Seq. ID No. 3826, Seq. ID No. 3842, Seq. ID No. 3856,
Seq. ID No. 3864, Seq. ID No. 3902, Seq. ID No. 3930, Seq. ID No. 4016, Seq.
ID No. 4018, Seq. ID No. 4056, Seq. ID No. 4076, Seq. ID No. 4086, Seq. ID No.
4090, Seq. ID No. 4100, Seq. ID No. 4106, Seq. ID No. 4130, Seq. ID No. 4204,
Seq. ID No. 4244, Seq. ID No. 4252, Seq. ID No. 4344, Seq. ID No. 4384, Seq.
30 ID No. 4476, Seq. ID No. 4482, Seq. ID No. 4488, Seq. ID No. 4492, Seq. ID No.
4534, Seq. ID No. 4628, Seq. ID No. 4706, Seq. ID No. 4714, Seq. ID No. 4718,
Seq. ID No. 4720, Seq. ID No. 4730, Seq. ID No. 4790, Seq. ID No. 4792, Seq.
ID No. 4794, Seq. ID No. 4804, Seq. ID No. 4814, Seq. ID No. 4816, Seq. ID No.

4826, Seq. ID No. 4834, Seq. ID No. 4838, Seq. ID No. 4876, Seq. ID No. 4880,
 Seq. ID No. 4920, Seq. ID No. 4932, Seq. ID No. 4948, Seq. ID No. 4986, Seq.
 ID No. 5078, Seq. ID No. 5116, Seq. ID No. 5118, Seq. ID No. 5128, Seq. ID No.
 5142, Seq. ID No. 5194, Seq. ID No. 5216, Seq. ID No. 5220, Seq. ID No. 5276,
 Seq. ID No. 5382, Seq. ID No. 5390, Seq. ID No. 5410, Seq. ID No. 5412, Seq.
 ID No. 5476, Seq. ID No. 5492, Seq. ID No. 5514, Seq. ID No. 5520, Seq. ID No.
 5526, Seq. ID No. 5530, Seq. ID No. 5538, Seq. ID No. 5558, Seq. ID No. 5582,
 Seq. ID No. 5600, Seq. ID No. 5638, Seq. ID No. 5686, Seq. ID No. 5724, Seq.
 ID No. 5756, Seq. ID No. 5762, Seq. ID No. 5896, Seq. ID No. 5902, Seq. ID No.
 5904, Seq. ID No. 5912, Seq. ID No. 5914, Seq. ID No. 5920, Seq. ID No. 5924,
 Seq. ID No. 5930, Seq. ID No. 6002, Seq. ID No. 6044, Seq. ID No. 6054, Seq.
 ID No. 6056, Seq. ID No. 6090, Seq. ID No. 6096, Seq. ID No. 6112, Seq. ID No.
 6118, Seq. ID No. 6166, Seq. ID No. 6170, Seq. ID No. 6188, Seq. ID No. 6196,
 Seq. ID No. 6220, Seq. ID No. 6234, Seq. ID No. 6270, Seq. ID No. 6276, Seq.
 ID No. 6280, Seq. ID No. 6288, Seq. ID No. 6298, Seq. ID No. 6300, Seq. ID No.
 6306, Seq. ID No. 6312, Seq. ID No. 6370, Seq. ID No. 6380, Seq. ID No. 6588,
 and Seq. ID No. 6592.

43. The *Alloiococcus otitidis* polypeptide of claim 36, wherein the polypeptide is
 identified using proteomics methodology as sharing homology with surface
 exposed proteins of *Streptococcus pneumoniae*, and is selected from one of Seq.
 ID No. 2, Seq. ID No. 6, Seq. ID No. 94, Seq. ID No. 96, Seq. ID No. 104, Seq. ID
 No. 108, Seq. ID No. 158, Seq. ID No. 224, Seq. ID No. 226, Seq. ID No. 234,
 Seq. ID No. 240, Seq. ID No. 254, Seq. ID No. 318, Seq. ID No. 322, Seq. ID No.
 342, Seq. ID No. 346, Seq. ID No. 354, Seq. ID No. 362, Seq. ID No. 364, Seq.
 ID No. 366, Seq. ID No. 376, Seq. ID No. 380, Seq. ID No. 384, Seq. ID No. 390,
 Seq. ID No. 392, Seq. ID No. 398, Seq. ID No. 406, Seq. ID No. 410, Seq. ID No.
 416, Seq. ID No. 424, Seq. ID No. 426, Seq. ID No. 428, Seq. ID No. 430, Seq.
 ID No. 436, Seq. ID No. 438, Seq. ID No. 440, Seq. ID No. 442, Seq. ID No. 444,
 Seq. ID No. 446, Seq. ID No. 448, Seq. ID No. 450, Seq. ID No. 462, Seq. ID No.
 464, Seq. ID No. 466, Seq. ID No. 514, Seq. ID No. 544, Seq. ID No. 552, Seq.
 ID No. 554, Seq. ID No. 560, Seq. ID No. 596, Seq. ID No. 602, Seq. ID No. 638,
 Seq. ID No. 650, Seq. ID No. 658, Seq. ID No. 670, Seq. ID No. 676, Seq. ID No.
 684, Seq. ID No. 754, Seq. ID No. 930, Seq. ID No. 970, Seq. ID No. 1042, Seq.

5 ID No. 1044, Seq. ID No. 1086, Seq. ID No. 1090, Seq. ID No. 1094, Seq. ID No.
1098, Seq. ID No. 1100, Seq. ID No. 1102, Seq. ID No. 1176, Seq. ID No. 1206,
Seq. ID No. 1238, Seq. ID No. 1460, Seq. ID No. 1496, Seq. ID No. 1498, Seq.
ID No. 1504, Seq. ID No. 1518, Seq. ID No. 1528, Seq. ID No. 1532, Seq. ID No.
1540, Seq. ID No. 1544, Seq. ID No. 1550, Seq. ID No. 1574, Seq. ID No. 1658,
Seq. ID No. 1710, Seq. ID No. 1768, Seq. ID No. 1786, Seq. ID No. 1822, Seq.
ID No. 1890, Seq. ID No. 1926, Seq. ID No. 1970, Seq. ID No. 2004, Seq. ID No.
2048, Seq. ID No. 2076, Seq. ID No. 2090, Seq. ID No. 2094, Seq. ID No. 2118,
Seq. ID No. 2138, Seq. ID No. 2144, Seq. ID No. 2206, Seq. ID No. 2236, Seq.
10 ID No. 2258, Seq. ID No. 2302, Seq. ID No. 2364, Seq. ID No. 2424, Seq. ID No.
2446, Seq. ID No. 2452, Seq. ID No. 2482, Seq. ID No. 2496, Seq. ID No. 2506,
Seq. ID No. 2578, Seq. ID No. 2588, Seq. ID No. 2614, Seq. ID No. 2634, Seq.
ID No. 2652, Seq. ID No. 2666, Seq. ID No. 2670, Seq. ID No. 2678, Seq. ID No.
2688, Seq. ID No. 2694, Seq. ID No. 2700, Seq. ID No. 2712, Seq. ID No. 2716,
15 Seq. ID No. 2758, Seq. ID No. 2792, Seq. ID No. 2794, Seq. ID No. 2804, Seq.
ID No. 2868, Seq. ID No. 2920, Seq. ID No. 2930, Seq. ID No. 3006, Seq. ID No.
3020, Seq. ID No. 3126, Seq. ID No. 3138, Seq. ID No. 3162, Seq. ID No. 3180,
Seq. ID No. 3252, Seq. ID No. 3260, Seq. ID No. 3286, Seq. ID No. 3310, Seq.
ID No. 3318, Seq. ID No. 3338, Seq. ID No. 3346, Seq. ID No. 3360, Seq. ID No.
20 3476, Seq. ID No. 3516, Seq. ID No. 3522, Seq. ID No. 3642, Seq. ID No. 3696,
Seq. ID No. 3794, Seq. ID No. 3902, Seq. ID No. 3928, Seq. ID No. 3988, Seq.
ID No. 4002, Seq. ID No. 4058, Seq. ID No. 4082, Seq. ID No. 4112, Seq. ID No.
4126, Seq. ID No. 4194, Seq. ID No. 4196, Seq. ID No. 4238, Seq. ID No. 4248,
Seq. ID No. 4384, Seq. ID No. 4394, Seq. ID No. 4398, Seq. ID No. 4402, Seq.
25 ID No. 4436, Seq. ID No. 4450, Seq. ID No. 4472, Seq. ID No. 4492, Seq. ID No.
4512, Seq. ID No. 4520, Seq. ID No. 4532, Seq. ID No. 4550, Seq. ID No. 4578,
Seq. ID No. 4582, Seq. ID No. 4586, Seq. ID No. 4610, Seq. ID No. 4612, Seq.
ID No. 4614, Seq. ID No. 4676, Seq. ID No. 4686, Seq. ID No. 4720, Seq. ID No.
4730, Seq. ID No. 4744, Seq. ID No. 4756, Seq. ID No. 4782, Seq. ID No. 4788,
30 Seq. ID No. 4838, Seq. ID No. 4842, Seq. ID No. 4850, Seq. ID No. 4856, Seq.
ID No. 4890, Seq. ID No. 4902, Seq. ID No. 4916, Seq. ID No. 4918, Seq. ID No.
4932, Seq. ID No. 4936, Seq. ID No. 4978, Seq. ID No. 5026, Seq. ID No. 5030,
Seq. ID No. 5110, Seq. ID No. 5116, Seq. ID No. 5118, Seq. ID No. 5156, Seq.

ID No. 5186, Seq. ID No. 5202, Seq. ID No. 5204, Seq. ID No. 5220, Seq. ID No. 5262, Seq. ID No. 5290, Seq. ID No. 5296, Seq. ID No. 5378, Seq. ID No. 5390, Seq. ID No. 5400, Seq. ID No. 5412, Seq. ID No. 5538, Seq. ID No. 5622, Seq. ID No. 5628, Seq. ID No. 5658, Seq. ID No. 5676, Seq. ID No. 5718, Seq. ID No. 5778, Seq. ID No. 5860, Seq. ID No. 5902, Seq. ID No. 5914, Seq. ID No. 5920, Seq. ID No. 5926, Seq. ID No. 5934, Seq. ID No. 6056, Seq. ID No. 6130, Seq. ID No. 6134, Seq. ID No. 6188, Seq. ID No. 6194, Seq. ID No. 6220, Seq. ID No. 6272, Seq. ID No. 6278, Seq. ID No. 6370, Seq. ID No. 6376, Seq. ID No. 6380, Seq. ID No. 6390, Seq. ID No. 6592, and Seq. ID No. 6606.

44. The *Alloiococcus otitidis* polypeptide of claim 36, wherein the polypeptide is identified as an *Alloiococcus otitidis* lipoprotein, and is selected from one Seq. ID No. 46, Seq. ID No. 48, Seq. ID No. 172, Seq. ID No. 226, Seq. ID No. 420, Seq. ID No. 514, Seq. ID No. 576, Seq. ID No. 592, Seq. ID No. 594, Seq. ID No. 658, Seq. ID No. 660, Seq. ID No. 670, Seq. ID No. 676, Seq. ID No. 746, Seq. ID No. 748, Seq. ID No. 936, Seq. ID No. 1046, Seq. ID No. 1076, Seq. ID No. 1138, Seq. ID No. 1174, Seq. ID No. 1192, Seq. ID No. 1194, Seq. ID No. 1196, Seq. ID No. 1564, Seq. ID No. 1662, Seq. ID No. 1664, Seq. ID No. 1666, Seq. ID No. 1792, Seq. ID No. 1798, Seq. ID No. 1918, Seq. ID No. 1970, Seq. ID No. 2116, Seq. ID No. 2160, Seq. ID No. 2430, Seq. ID No. 2528, Seq. ID No. 2700, Seq. ID No. 2816, Seq. ID No. 2876, Seq. ID No. 2976, Seq. ID No. 2978, Seq. ID No. 2992, Seq. ID No. 3044, Seq. ID No. 3324, Seq. ID No. 3338, Seq. ID No. 4134, Seq. ID No. 4138, Seq. ID No. 4482, Seq. ID No. 4706, Seq. ID No. 4828, Seq. ID No. 4870, Seq. ID No. 5116, Seq. ID No. 5378, Seq. ID No. 5380, Seq. ID No. 5492, Seq. ID No. 5510, Seq. ID No. 5514, Seq. ID No. 5526, Seq. ID No. 5530, Seq. ID No. 5532, Seq. ID No. 5890, Seq. ID No. 5910, Seq. ID No. 6026, Seq. ID No. 6028, Seq. ID No. 6088, Seq. ID No. 6090, Seq. ID No. 6326, Seq. ID No. 6328, Seq. ID No. 6416, Seq. ID No. 6638, Seq. ID No. 6640, and Seq. ID No. 6646.

45. The *Alloiococcus otitidis* polypeptide of claim 36, wherein the polypeptide is identified as having a LPXTG motif and is covalently attached to the peptidoglycan layer, and is selected from one of Seq. ID No. 504, Seq. ID No.

506, Seq. ID No. 1316, Seq. ID No. 1318, Seq. ID No. 1364, Seq. ID No. 1366, Seq. ID No. 1368, Seq. ID No. 1370, Seq. ID No. 1560, Seq. ID No. 1562, Seq. ID No. 1582, Seq. ID No. 1740, Seq. ID No. 1742, Seq. ID No. 2812, Seq. ID No. 2814, Seq. ID No. 3620, Seq. ID No. 5588, Seq. ID No. 5590, Seq. ID No. 5592, Seq. ID No. 5782, Seq. ID No. 5784, and Seq. ID No. 6104.

46. The *Alloiococcus otitidis* polypeptide of claim 36, wherein the polypeptide is identified as an *Alloiococcus otitidis* polypeptide, which is non-covalently associated with the peptidoglycan layer, and is selected from one of Seq. ID No. 3590, Seq. ID No. 3988, Seq. ID No. 5220, and Seq. ID No. 5338.

47. The *Alloiococcus otitidis* polypeptide of claim 36, wherein the polypeptide is identified as an *Alloiococcus otitidis* polypeptide having an RGD^X motif wherein X is not a proline residue and is selected from one of Seq. ID No. 38, Seq. ID No. 100, Seq. ID No. 108, Seq. ID No. 110, Seq. ID No. 112, Seq. ID No. 352, Seq. ID No. 354, Seq. ID No. 466, Seq. ID No. 468, Seq. ID No. 470, Seq. ID No. 472, Seq. ID No. 684, Seq. ID No. 822, Seq. ID No. 824, Seq. ID No. 1022, Seq. ID No. 1024, Seq. ID No. 1158, Seq. ID No. 1160, Seq. ID No. 1234, Seq. ID No. 1334, Seq. ID No. 1336, Seq. ID No. 1450, Seq. ID No. 1560, Seq. ID No. 1562, Seq. ID No. 1564, Seq. ID No. 1626, Seq. ID No. 1778, Seq. ID No. 1828, Seq. ID No. 1830, Seq. ID No. 1872, Seq. ID No. 1926, Seq. ID No. 2136, Seq. ID No. 2146, Seq. ID No. 2174, Seq. ID No. 2176, Seq. ID No. 2178, Seq. ID No. 2180, Seq. ID No. 2260, Seq. ID No. 2318, Seq. ID No. 2320, Seq. ID No. 2322, Seq. ID No. 2324, Seq. ID No. 2326, Seq. ID No. 2328, Seq. ID No. 2330, Seq. ID No. 2402, Seq. ID No. 2672, Seq. ID No. 2864, Seq. ID No. 2870, Seq. ID No. 2920, Seq. ID No. 2922, Seq. ID No. 2994, Seq. ID No. 3088, Seq. ID No. 3138, Seq. ID No. 3280, Seq. ID No. 3282, Seq. ID No. 3284, Seq. ID No. 3334, Seq. ID No. 3336, Seq. ID No. 3498, Seq. ID No. 3500, Seq. ID No. 3502, Seq. ID No. 3534, Seq. ID No. 3672, Seq. ID No. 3674, Seq. ID No. 3676, Seq. ID No. 3838, Seq. ID No. 3840, Seq. ID No. 3842, Seq. ID No. 3844, Seq. ID No. 3930, Seq. ID No. 3962, Seq. ID No. 4038, Seq. ID No. 4194, Seq. ID No. 4240, Seq. ID No. 4328, Seq. ID No. 4330, Seq. ID No. 4334, Seq. ID No. 4394, Seq. ID No. 4464, Seq. ID No. 4466, Seq. ID No. 4468, Seq. ID No. 4598, Seq. ID No. 4630, Seq. ID No.

4632, Seq. ID No. 4676, Seq. ID No. 4678, Seq. ID No. 4680, Seq. ID No. 4690,
Seq. ID No. 4692, Seq. ID No. 4694, Seq. ID No. 4782, Seq. ID No. 4800, Seq.
ID No. 4802, Seq. ID No. 4804, Seq. ID No. 4862, Seq. ID No. 5010, Seq. ID No.
5144, Seq. ID No. 5146, Seq. ID No. 5180, Seq. ID No. 5182, Seq. ID No. 5184,
5 Seq. ID No. 5250, Seq. ID No. 5252, Seq. ID No. 5254, Seq. ID No. 5260, Seq.
ID No. 5262, Seq. ID No. 5294, Seq. ID No. 5296, Seq. ID No. 5298, Seq. ID No.
5300, Seq. ID No. 5308, Seq. ID No. 5310, Seq. ID No. 5412, Seq. ID No. 5536,
Seq. ID No. 5538, Seq. ID No. 5746, Seq. ID No. 5822, Seq. ID No. 5824, Seq.
ID No. 5826, Seq. ID No. 6030, Seq. ID No. 6172, Seq. ID No. 6308, Seq. ID No.
10 6310, and Seq. ID No. 6312.

48. The *Alloicoccus otitidis* polypeptide of claim 36, wherein the polypeptide is
predicted by BlastP as being involved in capsule biosynthesis and transport, and
is selected from one of Seq. ID No. 50, Seq. ID No. 52, Seq. ID No. 54, Seq. ID
15 No. 60, Seq. ID No. 196, Seq. ID No. 690, Seq. ID No. 704, Seq. ID No. 926,
Seq. ID No. 1598, Seq. ID No. 1602, Seq. ID No. 1608, Seq. ID No. 1612, Seq.
ID No. 1614, Seq. ID No. 1714, Seq. ID No. 2030, Seq. ID No. 2264, Seq. ID No.
2270, Seq. ID No. 2374, Seq. ID No. 2438, Seq. ID No. 2652, Seq. ID No. 2768,
Seq. ID No. 2908, Seq. ID No. 3398, Seq. ID No. 3400, Seq. ID No. 3480, Seq.
20 ID No. 3488, Seq. ID No. 3492, Seq. ID No. 3494, Seq. ID No. 3496, Seq. ID No.
3498, Seq. ID No. 3520, Seq. ID No. 3522, Seq. ID No. 3530, Seq. ID No. 3536,
Seq. ID No. 3562, Seq. ID No. 3884, Seq. ID No. 3892, Seq. ID No. 3982, and
Seq. ID No. 4088.

49. The *Alloicoccus otitidis* polypeptide of claim 36, wherein the polynucleotide
encoding the polypeptide is predicted by BlastP as being localized in the capsule
loci region of *Alloicoccus otitidis*, and is selected from one of Seq. ID No. 46,
Seq. ID No. 48, Seq. ID No. 52, Seq. ID No. 54, Seq. ID No. 56, Seq. ID No. 58,
Seq. ID No. 60, Seq. ID No. 684, Seq. ID No. 686, Seq. ID No. 688, Seq. ID No.
25 690, Seq. ID No. 692, Seq. ID No. 694, Seq. ID No. 696, Seq. ID No. 698, Seq.
ID No. 700, Seq. ID No. 702, Seq. ID No. 704, Seq. ID No. 706, Seq. ID No. 708,
Seq. ID No. 710, Seq. ID No. 712, Seq. ID No. 714, Seq. ID No. 716, Seq. ID No.
30 718, Seq. ID No. 720, Seq. ID No. 722, Seq. ID No. 724, Seq. ID No. 726, Seq.

ID No. 728, Seq. ID No. 730, Seq. ID No. 732, Seq. ID No. 734, Seq. ID No. 736, Seq. ID No. 738, Seq. ID No. 740, Seq. ID No. 742, Seq. ID No. 744, Seq. ID No. 746, Seq. ID No. 748, Seq. ID No. 750, Seq. ID No. 752, Seq. ID No. 754, Seq. ID No. 3390, Seq. ID No. 3392, Seq. ID No. 3394, Seq. ID No. 3396, Seq. ID No. 3398, Seq. ID No. 3400, Seq. ID No. 3402, Seq. ID No. 3404, Seq. ID No. 3406, Seq. ID No. 3408, Seq. ID No. 3410, Seq. ID No. 3412, Seq. ID No. 3414, Seq. ID No. 3416, Seq. ID No. 3418, Seq. ID No. 3420, Seq. ID No. 3422, Seq. ID No. 3424, Seq. ID No. 3426, Seq. ID No. 3428, Seq. ID No. 3430, Seq. ID No. 3432, Seq. ID No. 3434, Seq. ID No. 3436, Seq. ID No. 3438, Seq. ID No. 3440, Seq. ID No. 3442, Seq. ID No. 3444, Seq. ID No. 3446, Seq. ID No. 3448, Seq. ID No. 3450, Seq. ID No. 3452, Seq. ID No. 3454, Seq. ID No. 3456, Seq. ID No. 3458, Seq. ID No. 3460, Seq. ID No. 3462, Seq. ID No. 3464, Seq. ID No. 3466, Seq. ID No. 3468, Seq. ID No. 3470, Seq. ID No. 3472, Seq. ID No. 3474, Seq. ID No. 3476, Seq. ID No. 3478, Seq. ID No. 3480, Seq. ID No. 3482, Seq. ID No. 3484, Seq. ID No. 3486, Seq. ID No. 3488, Seq. ID No. 3490, Seq. ID No. 3492, Seq. ID No. 3494, Seq. ID No. 3496, Seq. ID No. 3498, Seq. ID No. 3500, Seq. ID No. 3502, Seq. ID No. 3504, Seq. ID No. 3506, Seq. ID No. 3508, Seq. ID No. 3510, Seq. ID No. 3512, Seq. ID No. 3514, Seq. ID No. 3516, Seq. ID No. 3518, Seq. ID No. 3520, Seq. ID No. 3522, Seq. ID No. 3524, Seq. ID No. 3526, Seq. ID No. 3528, Seq. ID No. 3530, Seq. ID No. 3532, Seq. ID No. 3534, Seq. ID No. 3536, Seq. ID No. 3538, Seq. ID No. 3540, Seq. ID No. 3542, Seq. ID No. 3544, Seq. ID No. 3546, Seq. ID No. 3548, Seq. ID No. 3550, Seq. ID No. 3552, Seq. ID No. 3554, Seq. ID No. 3556, Seq. ID No. 3558, Seq. ID No. 3560, and Seq. ID No. 3562.

50. The *Alloiococcus otitidis* polypeptide of claim 36, wherein the polypeptide is predicted by BlastP to be associated with sporulation, and is selected from one of Seq. ID No. 1138, Seq. ID No. 1456, Seq. ID No. 2138, Seq. ID No. 2142, Seq. ID No. 2166, Seq. ID No. 2180, Seq. ID No. 2302, Seq. ID No. 2754, Seq. ID No. 4212, Seq. ID No. 4252, Seq. ID No. 4328, Seq. ID No. 4570, Seq. ID No. 4720, and Seq. ID No. 4730.

51. The *Alloiococcus otitidis* polypeptide of claim 36, wherein the polypeptide encoded by the polynucleotide is predicted by BlastP to be a unique polypeptide, and is selected from one of Seq. ID No. 8, Seq. ID No. 20, Seq. ID No. 22, Seq. ID No. 24, Seq. ID No. 32, Seq. ID No. 40, Seq. ID No. 66, Seq. ID No. 68, Seq. ID No. 70, Seq. ID No. 92, Seq. ID No. 100, Seq. ID No. 106, Seq. ID No. 114, Seq. ID No. 116, Seq. ID No. 124, Seq. ID No. 126, Seq. ID No. 128, Seq. ID No. 132, Seq. ID No. 134, Seq. ID No. 140, Seq. ID No. 152, Seq. ID No. 160, Seq. ID No. 162, Seq. ID No. 164, Seq. ID No. 166, Seq. ID No. 170, Seq. ID No. 186, Seq. ID No. 190, Seq. ID No. 194, Seq. ID No. 230, Seq. ID No. 232, Seq. ID No. 256, Seq. ID No. 258, Seq. ID No. 260, Seq. ID No. 276, Seq. ID No. 338, Seq. ID No. 340, Seq. ID No. 348, Seq. ID No. 350, Seq. ID No. 358, Seq. ID No. 360, Seq. ID No. 370, Seq. ID No. 372, Seq. ID No. 378, Seq. ID No. 386, Seq. ID No. 388, Seq. ID No. 394, Seq. ID No. 400, Seq. ID No. 402, Seq. ID No. 404, Seq. ID No. 408, Seq. ID No. 420, Seq. ID No. 432, Seq. ID No. 478, Seq. ID No. 496, Seq. ID No. 508, Seq. ID No. 520, Seq. ID No. 542, Seq. ID No. 546, Seq. ID No. 548, Seq. ID No. 550, Seq. ID No. 558, Seq. ID No. 590, Seq. ID No. 618, Seq. ID No. 620, Seq. ID No. 634, Seq. ID No. 640, Seq. ID No. 642, Seq. ID No. 644, Seq. ID No. 646, Seq. ID No. 648, Seq. ID No. 652, Seq. ID No. 654, Seq. ID No. 656, Seq. ID No. 668, Seq. ID No. 692, Seq. ID No. 694, Seq. ID No. 696, Seq. ID No. 698, Seq. ID No. 716, Seq. ID No. 718, Seq. ID No. 720, Seq. ID No. 732, Seq. ID No. 734, Seq. ID No. 742, Seq. ID No. 744, Seq. ID No. 746, Seq. ID No. 748, Seq. ID No. 750, Seq. ID No. 752, Seq. ID No. 756, Seq. ID No. 758, Seq. ID No. 760, Seq. ID No. 762, Seq. ID No. 764, Seq. ID No. 766, Seq. ID No. 768, Seq. ID No. 802, Seq. ID No. 804, Seq. ID No. 806, Seq. ID No. 808, Seq. ID No. 810, Seq. ID No. 812, Seq. ID No. 814, Seq. ID No. 834, Seq. ID No. 842, Seq. ID No. 850, Seq. ID No. 852, Seq. ID No. 854, Seq. ID No. 856, Seq. ID No. 888, Seq. ID No. 890, Seq. ID No. 892, Seq. ID No. 904, Seq. ID No. 906, Seq. ID No. 910, Seq. ID No. 938, Seq. ID No. 942, Seq. ID No. 944, Seq. ID No. 952, Seq. ID No. 958, Seq. ID No. 974, Seq. ID No. 976, Seq. ID No. 988, Seq. ID No. 1006, Seq. ID No. 1008, Seq. ID No. 1010, Seq. ID No. 1012, Seq. ID No. 1020, Seq. ID No. 1026, Seq. ID No. 1028, Seq. ID No. 1046, Seq. ID No. 1048, Seq. ID No. 1072, Seq. ID No. 1074, Seq. ID No. 1078, Seq. ID No. 1106, Seq. ID No. 1108, Seq. ID No. 1112, Seq. ID No. 1132, Seq. ID No. 1136, Seq. ID No. 1140,

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25 Seq. ID No. 1696, Seq. ID No. 1702, Seq. ID No. 1704, Seq. ID No. 1706, Seq.
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30 1832, Seq. ID No. 1852, Seq. ID No. 1858, Seq. ID No. 1876, Seq. ID No. 1900,
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2010, Seq. ID No. 2012, Seq. ID No. 2018, Seq. ID No. 2020, Seq. ID No. 2024,

Seq. ID No. 2026, Seq. ID No. 2028, Seq. ID No. 2040, Seq. ID No. 2042, Seq.
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5 ID No. 2146, Seq. ID No. 2156, Seq. ID No. 2158, Seq. ID No. 2160, Seq. ID No.
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15 2494, Seq. ID No. 2502, Seq. ID No. 2504, Seq. ID No. 2522, Seq. ID No. 2524,
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30 2936, Seq. ID No. 2938, Seq. ID No. 2940, Seq. ID No. 2942, Seq. ID No. 2944,
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5 ID No. 3124, Seq. ID No. 3152, Seq. ID No. 3154, Seq. ID No. 3168, Seq. ID No.
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10 Seq. ID No. 3246, Seq. ID No. 3248, Seq. ID No. 3250, Seq. ID No. 3262, Seq.
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52. The *Alloiococcus otitidis* polypeptide of claim 36, wherein the polypeptide is identified as an *Alloiococcus otitidis* polypeptide identified by Glimmer™ ORF finder program, and is selected from one of Seq. ID No. 2, Seq. ID No. 6, Seq. ID No. 12, Seq. ID No. 14, Seq. ID No. 16, Seq. ID No. 18, Seq. ID No. 26, Seq. ID No. 28, Seq. ID No. 30, Seq. ID No. 36, Seq. ID No. 38, Seq. ID No. 42, Seq. ID No. 44, Seq. ID No. 48, Seq. ID No. 52, Seq. ID No. 54, Seq. ID No. 60, Seq. ID No. 64, Seq. ID No. 70, Seq. ID No. 74, Seq. ID No. 76, Seq. ID No. 82, Seq. ID No. 84, Seq. ID No. 90, Seq. ID No. 94, Seq. ID No. 98, Seq. ID No. 104, Seq. ID No. 112, Seq. ID No. 122, Seq. ID No. 126, Seq. ID No. 130, Seq. ID No. 136, Seq. ID No. 138, Seq. ID No. 146, Seq. ID No. 150, Seq. ID No. 158, Seq. ID No. 168, Seq. ID No. 174, Seq. ID No. 184, Seq. ID No. 188, Seq. ID No. 190, Seq. ID No. 192, Seq. ID No. 196, Seq. ID No. 198, Seq. ID No. 204, Seq. ID No. 208, Seq. ID No. 216, Seq. ID No. 220, Seq. ID No. 224, Seq. ID No. 226, Seq. ID No. 228, Seq. ID No. 232, Seq. ID No. 234, Seq. ID No. 240, Seq. ID No. 242, Seq. ID No. 248, Seq. ID No. 254, Seq. ID No. 262, Seq. ID No. 266, Seq. ID No. 270, Seq. ID No. 274, Seq. ID No. 276, Seq. ID No. 278, Seq. ID No. 284, Seq. ID No. 292, Seq. ID No. 294, Seq. ID No. 298, Seq. ID No. 302, Seq. ID No. 308, Seq. ID No. 310, Seq. ID No. 314, Seq. ID No. 318, Seq. ID No. 322, Seq. ID No. 326, Seq. ID No. 336, Seq. ID No. 344, Seq. ID No. 346, Seq. ID No. 354, Seq. ID No.

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- 5 53. The *Alloiococcus otitidis* polypeptide of claim 36, wherein the polypeptide is identified as an *Alloiococcus otitidis* polypeptide by GeneMark™ ORF finder program, and is selected from one of Seq. ID No. 2, Seq. ID No. 4, Seq. ID No. 12, Seq. ID No. 14, Seq. ID No. 16, Seq. ID No. 18, Seq. ID No. 26, Seq. ID No. 28, Seq. ID No. 30, Seq. ID No. 36, Seq. ID No. 38, Seq. ID No. 40, Seq. ID No. 42, Seq. ID No. 44, Seq. ID No. 46, Seq. ID No. 50, Seq. ID No. 54, Seq. ID No. 58, Seq. ID No. 62, Seq. ID No. 70, Seq. ID No. 72, Seq. ID No. 76, Seq. ID No. 82, Seq. ID No. 84, Seq. ID No. 90, Seq. ID No. 96, Seq. ID No. 102, Seq. ID No. 112, Seq. ID No. 120, Seq. ID No. 126, Seq. ID No. 130, Seq. ID No. 136, Seq. ID No. 138, Seq. ID No. 142, Seq. ID No. 148, Seq. ID No. 152, Seq. ID No. 156, Seq. ID No. 168, Seq. ID No. 172, Seq. ID No. 182, Seq. ID No. 186, Seq. ID No. 188, Seq. ID No. 190, Seq. ID No. 192, Seq. ID No. 196, Seq. ID No. 200, Seq. ID No. 208, Seq. ID No. 214, Seq. ID No. 220, Seq. ID No. 222, Seq. ID No. 226, Seq. ID No. 228, Seq. ID No. 230, Seq. ID No. 234, Seq. ID No. 240, Seq. ID No. 242, Seq. ID No. 244, Seq. ID No. 254, Seq. ID No. 262, Seq. ID No. 264, Seq. ID No. 268, Seq. ID No. 274, Seq. ID No. 276, Seq. ID No. 278, Seq. ID No. 280, Seq. ID No. 292, Seq. ID No. 294, Seq. ID No. 296, Seq. ID No. 300, Seq. ID No. 304, Seq. ID No. 310, Seq. ID No. 312, Seq. ID No. 316, Seq. ID No. 320, Seq. ID No. 324, Seq. ID No. 332, Seq. ID No. 342, Seq. ID No. 346, Seq. ID No. 352, Seq. ID No. 356, Seq. ID No. 362, Seq. ID No. 364, Seq. ID No. 366, Seq. ID No. 376, Seq. ID No. 380, Seq. ID No. 382, Seq. ID No. 384, Seq. ID No. 390, Seq. ID No. 392, Seq. ID No. 396, Seq. ID No. 400, Seq. ID No. 406, Seq. ID No. 410, Seq. ID No. 414, Seq. ID No. 418, Seq. ID No. 422, Seq. ID No. 424, Seq. ID No. 426, Seq. ID No. 428, Seq. ID No. 430, Seq. ID No. 436, Seq. ID No. 438, Seq. ID No. 440, Seq. ID No. 442, Seq. ID No. 444, Seq. ID No. 446, Seq. ID No. 448, Seq. ID No. 450, Seq. ID No. 460, Seq. ID No. 466, Seq. ID No. 486, Seq. ID No. 502, Seq. ID No. 506, Seq. ID No. 512, Seq. ID No. 514, Seq. ID No. 518, Seq. ID No. 520, Seq. ID No. 524, Seq. ID No. 530, Seq. ID No. 534, Seq. ID No. 536, Seq. ID No. 542, Seq. ID No. 544, Seq. ID No. 552, Seq. ID No. 554, Seq. ID No.

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54. The *Alloiococcus otitidis* polypeptide of claim 36, wherein the polypeptide is identified as an *Alloiococcus otitidis* polypeptide identified by an ORF finder program that searches for an ATG, GTG or TTG start codon between a Stop-Stop region, and is selected from one of Seq. ID No. 2, Seq. ID No. 6, Seq. ID No. 12, Seq. ID No. 14, Seq. ID No. 16, Seq. ID No. 18, Seq. ID No. 20, Seq. ID

No. 22, Seq. ID No. 24, Seq. ID No. 28, Seq. ID No. 30, Seq. ID No. 32, Seq. ID
No. 36, Seq. ID No. 38, Seq. ID No. 42, Seq. ID No. 44, Seq. ID No. 46, Seq. ID
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ID No. 6604, Seq. ID No. 6606, Seq. ID No. 6610, Seq. ID No. 6612, Seq. ID No. 6614, Seq. ID No. 6616, Seq. ID No. 6618, Seq. ID No. 6620, Seq. ID No. 6622, Seq. ID No. 6624, Seq. ID No. 6628, Seq. ID No. 6630, Seq. ID No. 6632, Seq. ID No. 6634, Seq. ID No. 6638, Seq. ID No. 6640, Seq. ID No. 6644, Seq. ID No. 6646, and Seq. ID No. 6650.

55. The *Alloiococcus otitidis* polypeptide of claim 36, wherein the polypeptide is identified by an ORF finder program that searches for a transmembrane domain between two Stop codons and a Start codon immediately upstream of this transmembrane region, and is selected from one of Seq. ID No. 8, Seq. ID No. 10, Seq. ID No. 34, Seq. ID No. 48, Seq. ID No. 68, Seq. ID No. 86, Seq. ID No. 88, Seq. ID No. 124, Seq. ID No. 134, Seq. ID No. 142, Seq. ID No. 160, Seq. ID No. 164, Seq. ID No. 192, Seq. ID No. 210, Seq. ID No. 212, Seq. ID No. 216, Seq. ID No. 218, Seq. ID No. 226, Seq. ID No. 236, Seq. ID No. 238, Seq. ID No. 250, Seq. ID No. 252, Seq. ID No. 256, Seq. ID No. 272, Seq. ID No. 278, Seq. ID No. 286, Seq. ID No. 288, Seq. ID No. 290, Seq. ID No. 328, Seq. ID No. 330, Seq. ID No. 374, Seq. ID No. 376, Seq. ID No. 420, Seq. ID No. 488, Seq. ID No. 498, Seq. ID No. 500, Seq. ID No. 504, Seq. ID No. 506, Seq. ID No. 510, Seq. ID No. 512, Seq. ID No. 516, Seq. ID No. 526, Seq. ID No. 528, Seq. ID No. 546, Seq. ID No. 568, Seq. ID No. 570, Seq. ID No. 576, Seq. ID No. 578, Seq. ID No. 580, Seq. ID No. 594, Seq. ID No. 618, Seq. ID No. 638, Seq. ID No. 640, Seq. ID No. 642, Seq. ID No. 646, Seq. ID No. 654, Seq. ID No. 656, Seq. ID No. 660, Seq. ID No. 670, Seq. ID No. 676, Seq. ID No. 678, Seq. ID No. 680, Seq. ID No. 716, Seq. ID No. 718, Seq. ID No. 720, Seq. ID No. 722, Seq. ID No. 724, Seq. ID No. 748, Seq. ID No. 752, Seq. ID No. 756, Seq. ID No. 758, Seq. ID No. 760, Seq. ID No. 762, Seq. ID No. 764, Seq. ID No. 770, Seq. ID No. 778, Seq. ID No. 780, Seq. ID No. 808, Seq. ID No. 810, Seq. ID No. 820, Seq. ID No. 826, Seq. ID No. 864, Seq. ID No. 894, Seq. ID No. 902, Seq. ID No. 936, Seq. ID No. 944, Seq. ID No. 956, Seq. ID No. 968, Seq. ID No. 980, Seq. ID No. 1006, Seq. ID No. 1010, Seq. ID No. 1012, Seq. ID No. 1014, Seq. ID No. 1016, Seq. ID No. 1020, Seq. ID No. 1030, Seq. ID No. 1032, Seq. ID No. 1034, Seq. ID No. 1038, Seq. ID No. 1040, Seq. ID No. 1046, Seq. ID No. 1056, Seq. ID No. 1076, Seq. ID No. 1106, Seq. ID No. 1132, Seq. ID No. 1136, Seq. ID No. 1138, Seq. ID No.

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ID No. 6582, Seq. ID No. 6594, Seq. ID No. 6600, Seq. ID No. 6632, and Seq. ID
No. 6640.

20 56. An isolated polypeptide encoded by a polynucleotide comprising a nucleotide
sequence having at least about 70% identity to a nucleotide sequence contained
within SEQ ID NO: 6651, a complement thereof, a degenerate variant thereof,
and a fragment thereof. ✓

25 57. A recombinant expression vector comprising a nucleotide sequence having at
least about 70% identity to a nucleotide sequence chosen from one of the odd
numbered sequences set out in SEQ ID NO: 1 through SEQ ID NO: 6649, a
complement thereof, a degenerate variant thereof, and a fragment thereof. ✓

30 58. The vector of claim 57, wherein the polynucleotide is selected from the group
consisting of genomic DNA, cDNA, and RNA.

59. The vector of claim 58, wherein the polynucleotide comprises heterologous nucleotide sequences.

5 60. The vector of claim 58, wherein the polynucleotide is operatively linked to one or more gene expression regulatory elements.

10 61. The vector of claim 60, wherein the polynucleotide encodes a polypeptide comprising an amino acid sequence having at least about 70% identity to an amino acid sequence chosen from one of even numbered sequences set out in SEQ ID NO: 2 through SEQ ID NO: 6650, a biological equivalent thereof, and a fragment thereof.

62. The vector of claim 57, wherein the vector is a plasmid.

15 63. A genetically engineered host cell, transfected, transformed or infected with the vector of claim 57.

64. The host cell of claim 63, wherein the host cell is a bacterial cell.

20 65. The host cell of claim 64, wherein the polynucleotide is expressed to produce the encoded polypeptide, a biological equivalent thereof, or a fragment thereof.

25 66. An antibody specific for a polypeptide encoded by an *Alloiococcus otitidis* polynucleotide chosen from one of the odd numbered sequences from SEQ ID NO: 1 through SEQ ID NO: 6649, a complement thereof, a fragment thereof, and a degenerate variant thereof. ✓

30 67. An antibody specific for an *Alloiococcus otitidis* polypeptide chosen from one of even numbered sequence listings set out in SEQ ID NO: 2 through SEQ ID NO: 6650, a complement thereof, a biological equivalent thereof, and a fragment thereof. ✓

68. The antibody of claim 66, wherein the antibody is selected from the group consisting of monoclonal, polyclonal, chimeric, humanized and single chain.
- 5 69. The antibody of claim 67, wherein the antibody is selected from the group consisting of monoclonal, polyclonal, chimeric, humanized and single chain.
70. The antibody of claim 66, wherein the antibody is monoclonal.
71. The antibody of claim 67, wherein the antibody is monoclonal.
- 10 72. The antibody of claim 66, wherein the antibody is humanized.
73. The antibody of claim 67, wherein the antibody is humanized.
- 15 74. An immunogenic composition comprising a polypeptide having an amino acid sequence chosen from one of even numbered sequence listings set out in SEQ ID NO: 2 through SEQ ID NO: 6650, a complement thereof, a biological equivalent thereof, and a fragment thereof. ✓
- 20 75. The immunogenic composition of claim 74, further comprising a pharmaceutically acceptable carrier.
76. The immunogenic composition of claim 74, further comprising one or more adjuvants.
- 25 77. The immunogenic composition of claim 74, wherein the polypeptide is further defined as:
- 30 (a) an *Alloiococcus otitidis* polypeptide predicted by SignalP algorithm analysis as having met all four criteria set out in the SignalP algorithm for a polypeptide having a signal peptide and predicted by HMM Signal P algorithm analysis as having a signal peptide;
- (b) an *Alloiococcus otitidis* polypeptide predicted by SignalP algorithm analysis as having met three of the four criteria set out in the SignalP

algorithm for a polypeptide having a signal peptide and predicted by HMM Signal P algorithm analysis as having a signal peptide;

(c) an *Alloiococcus otitidis* polypeptide predicted by HMM SignalP algorithm analysis as having a signal peptide;

5 (d) an *Alloiococcus otitidis* polypeptide predicted by HMM SignalP algorithm analysis as being a non-secretory protein;

(e) an *Alloiococcus otitidis* polypeptide identified by BlastP analysis;

(f) an *Alloiococcus otitidis* polypeptide identified by Pfam analysis;

10 (g) an *Alloiococcus otitidis* polypeptide identified using proteomics methodology as sharing homology with surface exposed proteins of *Streptococcus pneumoniae*;

(h) an *Alloiococcus otitidis* lipoprotein;

(i) an *Alloiococcus otitidis* polypeptide having a LPXTG motif, wherein the polypeptide is covalently attached to the peptidoglycan layer;

15 (j) an *Alloiococcus otitidis* polypeptide, wherein the polypeptide is non-covalently associated with the peptidoglycan layer;

(k) an *Alloiococcus otitidis* polypeptide having an RGD_X motif wherein X is not a proline residue;

20 (l) an *Alloiococcus otitidis* polypeptide predicted by BlastP as being involved in capsule biosynthesis and transport;

(m) an *Alloiococcus otitidis* polypeptide identified by BlastP as being localized within the capsule loci of the *Alloiococcus otitidis* genome;

(n) an *Alloiococcus otitidis* polypeptide predicted by BlastP as being associated with sporulation;

25 (o) an *Alloiococcus otitidis* polypeptide encoded by unique ORFs identified by BlastP analysis as having a BlastP 'E Value' of $> e^{-10}$;

(p) an *Alloiococcus otitidis* polypeptide identified by Glimmer™ ORF finder program;

30 (q) an *Alloiococcus otitidis* polypeptide identified by GeneMark™ ORF finder program;

(r) an *Alloiococcus otitidis* polypeptide identified by an ORF finder program that searches for an ATG, GTG or TTG start codon between a Stop-Stop region; and

- (s) an *Alloiococcus otitidis* polypeptide identified by an ORF finder program that searches for a transmembrane domain between two Stop codons and a Stop codon immediately upstream of this transmembrane region.

- 5 78. The immunogenic composition of claim 77, wherein the polypeptide further comprises heterologous amino acids.
79. The immunogenic composition of claim 77, wherein the polypeptide is a fusion polypeptide.
- 10 80. The immunogenic composition of claim 77, wherein the polypeptide is encoded by a polynucleotide comprising a nucleotide sequence having at least about 70% identity to a nucleotide sequence chosen from one of odd numbered sequence listings set out in SEQ ID NO: 1 through SEQ ID NO: 6649, a degenerate variant thereof, or a fragment thereof.
- 15 81. The immunogenic composition of claim 80, wherein the polynucleotide further comprises heterologous nucleotides.
- 20 82. An immunogenic composition comprising a polynucleotide having a nucleotide sequence chosen from one of one of odd numbered sequence listings set out in SEQ ID NO: 1 through SEQ ID NO: 6649, a degenerate variant thereof, or a fragment thereof and is comprised in an expression vector.
- 25 83. The immunogenic composition of claim 82, wherein the vector is plasmid DNA.
84. The immunogenic composition of claim 83, wherein the polynucleotide comprises heterologous nucleotides.
- 30 85. The immunogenic composition of claim 83, wherein the polynucleotide is operatively linked to one or more gene expression regulatory elements.

86. The immunogenic composition of claim 85, wherein the polynucleotide directs the expression of a neutralizing epitope of *Alloiococcus otitidis*.
87. The immunogenic composition of claim 86, further comprising one or more adjuvants.
88. A pharmaceutical composition comprising a polypeptide and a pharmaceutically acceptable carrier, wherein the polypeptide comprises an amino acid chosen from one of even numbered sequence listings set out in SEQ ID NO: 2 through SEQ ID NO: 6650, a complement thereof, a biological equivalent thereof, and a fragment thereof.
89. The pharmaceutical composition of claim 88, wherein the polypeptide is further defined as:
- (a) an *Alloiococcus otitidis* polypeptide predicted by SignalP algorithm analysis as having met all four criteria set out in the SignalP algorithm for a polypeptide having a signal peptide and predicted by HMM SignalP algorithm analysis as having a signal peptide;
 - (b) an *Alloiococcus otitidis* polypeptide predicted by SignalP algorithm analysis as having met three of the four criteria set out in the SignalP algorithm for a polypeptide having a signal peptide and predicted by HMM SignalP algorithm analysis as having a signal peptide;
 - (c) an *Alloiococcus otitidis* polypeptide predicted by HMM SignalP algorithm analysis as having a signal peptide;
 - (d) an *Alloiococcus otitidis* polypeptide predicted by HMM SignalP algorithm analysis as being a non-secretory protein;
 - (e) an *Alloiococcus otitidis* polypeptide identified by BlastP analysis;
 - (f) an *Alloiococcus otitidis* polypeptide identified by Pfam analysis;
 - (g) an *Alloiococcus otitidis* polypeptide identified using proteomics methodology as sharing homology with surface exposed proteins of *Streptococcus pneumoniae*;
 - (h) an *Alloiococcus otitidis* lipoprotein;

- 5 (i) an *Alloiococcus otitidis* polypeptide having a LPXTG motif, wherein the polypeptide is covalently attached to the peptidoglycan layer;
- (j) an *Alloiococcus otitidis* polypeptide, wherein the polypeptide is non-covalently associated with the peptidoglycan layer;
- 10 (k) an *Alloiococcus otitidis* polypeptide having an RGDX motif wherein X is not a proline residue;
- (l) an *Alloiococcus otitidis* polypeptide predicted by BlastP as being involved in capsule biosynthesis and transport;
- (m) an *Alloiococcus otitidis* polypeptide identified by BlastP as being localized within the capsule loci of the *Alloiococcus otitidis* genome;
- 15 (n) an *Alloiococcus otitidis* polypeptide predicted by BlastP as being associated with sporulation;
- (o) an *Alloiococcus otitidis* polypeptide encoded by unique ORFs identified by BlastP analysis as having a BlastP 'E Value' of $> e^{-10}$;
- 20 (p) an *Alloiococcus otitidis* polypeptide identified by Glimmer™ ORF finder program;
- (q) an *Alloiococcus otitidis* polypeptide identified by GeneMark™ ORF finder program;
- (r) an *Alloiococcus otitidis* polypeptide identified by an ORF finder program that searches for an ATG, GTG or TTG start codon between a Stop-Stop region; and
- 25 (s) an *Alloiococcus otitidis* polypeptide identified by an ORF finder program that searches for a transmembrane domain between two Stop codons and a Start codon immediately upstream of this transmembrane region.
90. The pharmaceutical composition of claim 89, wherein the polypeptide further comprises heterologous amino acids.
91. The pharmaceutical composition of claim 90, wherein the polypeptide is a fusion polypeptide.
92. A DNA chip comprising an array of polynucleotides, wherein at least one of the polynucleotides comprise a nucleotide sequence chosen from one of one of odd

numbered sequence listings set out in SEQ ID NO: 1 through SEQ ID NO: 6649, a complement thereof, a degenerate variant thereof, and a fragment thereof.

- 5 93. A protein chip comprising an array of polypeptides, wherein at least one of the polypeptides comprises an amino acid sequence chosen from one of even numbered sequence listings set out in SEQ ID NO: 2 through SEQ ID NO: 6650, a biological equivalent thereof, or a fragment thereof.
- 10 94. A method of immunizing against *Alloicoccus otitidis* comprising administering to a host an immunizing amount of an immunogenic composition comprising a polypeptide and a pharmaceutically acceptable carrier, wherein the polypeptide comprises an amino acid sequence chosen from one of even numbered sequence listings set out in SEQ ID NO: 2 through SEQ ID NO: 6650, a biological equivalent thereof, or a fragment thereof.
- 15 95. The method of claim 94, wherein the polypeptide is a fusion polypeptide.
96. The method of claim 94, further comprising an adjuvant.
- 20 97. A method for the detection and/or identification of *Alloicoccus otitidis* in a biological sample comprising:
- 25 (a) contacting the sample with an oligonucleotide probe of a polynucleotide comprising the nucleotide sequence chosen from one of odd numbered sequence listings set out in SEQ ID NO: 1 through SEQ ID NO: 6649, a degenerate variant thereof, or a fragment thereof, under conditions permitting hybridization; and
- (b) detecting the presence of hybridization complexes in the sample, wherein hybridization complexes indicate the presence of *Alloicoccus otitidis* in the sample.
- 30 98. A method for the detection and/or identification of *Alloicoccus otitidis* in a biological sample comprising:

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- (a) contacting the sample with an oligonucleotide primer of a polynucleotide comprising the nucleotide sequence chosen from one of odd numbered sequence listings set out in SEQ ID NO: 1 through SEQ ID NO: 6649, a degenerate variant thereof, or a fragment thereof, in the presence of nucleotides and a polymerase enzyme under conditions permitting primer extension; and
 - (b) detecting the presence of primer extension products in the sample, wherein extension products indicate the presence of *Alloiococcus otitidis* in the sample.

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99. A method for the detection and/or identification of *Alloiococcus otitidis* in a biological sample comprising: ✓

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- (a) contacting the sample with an antibody specific for a polypeptide comprising an amino acid sequence chosen from one of even numbered sequence listings set out in SEQ ID NO: 2 through SEQ ID NO: 6650, a biological equivalent thereof, or a fragment thereof, under conditions permitting immune complex formation; and
- (b) detecting the presence of immune complexes in the sample, wherein immune complexes indicate the presence of *Alloiococcus otitidis* in the sample.

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100. A method for the detection and/or identification of antibodies to *Alloiococcus otitidis* in a biological sample comprising: ✓

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- (a) contacting the sample with a polypeptide comprising an amino acid sequence chosen from one of even numbered sequence listings set out in SEQ ID NO: 2 through SEQ ID NO: 6650, a biological equivalent thereof, or a fragment thereof, under conditions permitting immune complex formation; and
- (b) detecting the presence of immune complexes in the sample, wherein immune complexes indicate the presence of *Alloiococcus otitidis* in the sample.

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101. A kit comprising a container containing an isolated polynucleotide comprising an nucleotide sequence chosen from one of odd numbered sequence listing set out in SEQ ID NO: 1 through SEQ ID NO: 6649, a degenerate variant thereof, or a fragment thereof. ✓
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102. The kit of claim 101, wherein the polynucleotide is a primer or a probe.
103. The kit of claim 101, wherein the polynucleotide is a primer and the kit further comprises a container containing a polymerase.
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104. The kit of claim 103, wherein the kit further comprises a container containing dNTP.
105. A kit comprising a container containing an antibody that immunospecifically binds to a polypeptide comprising the amino acid sequence chosen from one of even numbered sequence listings set out in SEQ ID NO: 2 through SEQ ID NO: 6650, a biological equivalent thereof, or a fragment thereof. ✓
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106. A kit comprising a container containing an antibody that immunospecifically binds to a fusion polypeptide comprising at least the amino acid sequence chosen from one of even numbered sequence listings set out in SEQ ID NO: 2 through SEQ ID NO: 6650, a biological equivalent thereof, or a fragment thereof. ✓
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107. A method for producing a polypeptide, which comprises culturing the genetically engineered host cell of claim 63 under conditions suitable to produce the polypeptide and recovering the polypeptide from the culture.
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